



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification 6 : <b>G01N 33/574</b></p>	<p><b>A2</b></p>	<p>(11) International Publication Number: <b>WO 99/04265</b></p> <p>(43) International Publication Date: <b>28 January 1999 (28.01.99)</b></p>																	
<p>(21) International Application Number: <b>PCT/US98/14679</b></p> <p>(22) International Filing Date: <b>15 July 1998 (15.07.98)</b></p> <p>(30) Priority Data:</p> <table style="width: 100%;"> <tr> <td style="width: 30%;">08/896,164</td> <td style="width: 40%;">17 July 1997 (17.07.97)</td> <td style="width: 30%;">US</td> </tr> <tr> <td>60/061,599</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>60/061,765</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>08/948,705</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>9721697.2</td> <td>11 October 1997 (11.10.97)</td> <td>GB</td> </tr> <tr> <td>09/102,322</td> <td>22 June 1998 (22.06.98)</td> <td>US</td> </tr> </table> <p>(71) Applicant (for all designated States except US): <b>LUDWIG INSTITUTE FOR CANCER RESEARCH [CH/US]; 605 Third Avenue, New York, NY 10158 (US).</b></p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): <b>OLD, Lloyd, J. [US/US]; 1345 Avenue of the Americas, New York, NY 10105 (US). SCANLAN, Matthew, J. [US/US]; 1275 York Avenue, New York, NY 10021 (US). STOCKERT, Elisabeth [US/US]; 1275 York Avenue, New York, NY 10021 (US). GURE, Ali [US/US]; 1275 York Avenue, New York, NY 10021 (US). CHEN, Yao-Tseng [-/US]; The New York Hospital-Cornell Medical Center, Dept. of Pathology, 525 East 68th Street, New York, NY 10021 (US). GOUT, Ivan</b></p>	08/896,164	17 July 1997 (17.07.97)	US	60/061,599	10 October 1997 (10.10.97)	US	60/061,765	10 October 1997 (10.10.97)	US	08/948,705	10 October 1997 (10.10.97)	US	9721697.2	11 October 1997 (11.10.97)	GB	09/102,322	22 June 1998 (22.06.98)	US	<p>[UA/GB]; 91 Riding House Street, London W1P 8BT (GB). O'HARE, Michael [GB/GB]; 91 Riding House Street, London W1P 8BT (GB). OBATA, Yuichi [JP/JP]; Chikusa-Ku, Nagoya 464 (JP). PFREUNDSCUHL, Michael [DE/DE]; Innere Medizin 1, D-66421 Homburg/Saar (DE). TURECI, Ozlem [DE/DE]; Innere Medizin 1, D-66421 Homburg/Saar (DE). SAHIN, Ugur [TR/DE]; Innere Medizin 1, D-66421 Homburg/Saar (DE).</p> <p>(74) Agent: <b>VAN AMSTERDAM, John, R.; Wolf, Greenfield &amp; Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).</b></p> <p>(81) Designated States: <b>AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO</b> patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p>
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<p><b>Published</b></p> <p><i>Without international search report and to be republished upon receipt of that report.</i></p>																			
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<p>(57) Abstract</p> <p>Various molecules associated with cancer are disclosed. The invention also discloses diagnostic and therapeutic methods based upon these molecules.</p>																			

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## **CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES**

### **Field of the Invention**

The invention relates to nucleic acids and encoded polypeptides which are cancer  
5 associated antigens expressed in patients afflicted with breast cancer. The invention also relates  
to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules,  
polypeptides coded for by such molecules and peptides derived therefrom, as well as related  
antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic  
contexts.

10

### **Background of the Invention**

The mechanism by which T cells recognize foreign materials has been implicated in  
cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous  
melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been  
15 described. In many instances, the antigens recognized by these clones have been  
characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells  
which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL  
clones which recognize the antigen-expressing cells can be isolated and propagated. While this  
20 approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers  
including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc.  
Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera  
are used to identify immunogenic protein antigens expressed in cancer cells by screening  
25 expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified  
have been found to have elicited a high-titer humoral immune response in the patients from  
which the antisera were obtained. Such a high-titer IgG response implies helper T cell  
recognition of the detected antigen. These tumor antigens can then be screened for the presence  
of MHC/HLA class I and class II motifs and reactivity with CTLs

30

The invention is elaborated upon in the disclosure which follows.

### Summary of the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those  
5 molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of  
10 conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments  
15 thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be  
20 used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a  
25 plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such  
30 combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses,

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer.

- 5 Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

- 15 In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

5 In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional  
10 variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer  
15 associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a different human cancer associated antigen or  
20 functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

25 According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other  
30 embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

5       The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid  
10   molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated  
15   nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

20       In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA  
25   binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA  
30   Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

5       The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a sequence of  
10       contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1, (2) complements of (1), and (3) fragments of (1) and (2).

      In one embodiment the sequence of contiguous nucleotides is selected from the group  
15       consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2) at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical  
20       to the sequence Group 1.

      In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18  
nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30  
nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides  
25       and every integer length therebetween.

      In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

      Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

30       According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described  
5 above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the  
10 isolated nucleic acid molecules the invention, described above, is provided. These include PP Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a human antibody.

The invention includes in another aspect an isolated fragment of a human cancer  
15 associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length  
20 to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from  
25 the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

30 According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent,



which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by  
5 the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected  
10 host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC  
15 molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to  
20 render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated  
25 antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the  
30 step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

10 The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (i) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

20 In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

30 The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter  
5 includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the  
10 complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular medicament is for  
15 treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal cancer, colon cancer, prostate cancer or gastric cancer.

### **Detailed Description of the Invention**

In the above summary and in the ensuing description, lists of sequences are provided.  
20 The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the  
25 sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the  
30 coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not known that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

#### "Nucleic Acid Sequences"

30 NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

5 (d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

10

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor,

15

(b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

20

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

25

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

30

NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

30

#### Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

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- PP Group 2. Polypeptides encoded by NA Group 2
- PP Group 3. Polypeptides encoded by NA Group 3.
- PP Group 4. Polypeptides encoded by NA Group 4.
- PP Group 5. Polypeptides encoded by NA Group 5.
- 5 PP Group 6. Polypeptides encoded by NA Group 6.
- PP Group 7. Polypeptides encoded by NA Group 7.
- PP Group 8. Polypeptides encoded by NA Group 8.
- PP Group 9. Polypeptides encoded by NA Group 9.
- PP Group 10. Polypeptides encoded by NA Group 10.
- 10 PP Group 11. Polypeptides encoded by NA Group 11.
- PP Group 12. Polypeptides encoded by NA Group 12.
- PP Group 13. Polypeptides encoded by NA Group 13.
- PP Group 14. Polypeptides encoded by NA Group 14.
- PP Group 15. Polypeptides encoded by NA Group 15.
- 15 PP Group 16. Polypeptides encoded by NA Group 16.
- PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH<sub>2</sub>PO<sub>4</sub>(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

30 There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to



manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by  
5 isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60%  
10 nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (<ftp://ncbi.nlm.nih.gov/pub/>). Exemplary tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov>. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained  
15 using the MacVetor sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect  
20 the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences  
25 presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs: [31, 33 and 34], which were found to react with allogeneic breast  
30 cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674.

5 The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of  
10 diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of  
15 diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those,  
20 which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of  
25 encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA,  
30 CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger  
5 nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank  
10 accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing  
15 GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

20 Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating  
25 antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic  
30 purposes as described in greater detail below.

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As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.,* Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generated individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990). for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient (for examples of this, see the Examples below).

Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

*Immunol.* 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

5 In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the  
10 vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a  
15 cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

20 As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of  
25 one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby,  
30 inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

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are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

5 In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which  
10 (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters,  
15 alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamides, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other  
20 than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding  
25 breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense  
30 oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term



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“pharmaceutically acceptable” means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term “physiologically acceptable” refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a “vector” may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g.,  $\beta$ -galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be “operably” joined

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when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

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human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 $\alpha$ , which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and partial

proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

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a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

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a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g., *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amaro and Drijfhout (D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

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molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant



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negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The

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pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')<sub>2</sub> fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for F(ab')<sub>2</sub>, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

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human or non-human sequences; chimeric F(ab')<sub>2</sub> fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer

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associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for  
5 example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics  
10 including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens  
15 disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminogluthethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- $\alpha$ , lomustine, mercaptopurine, methotrexate,  
20 mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein,  
25 cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer  
30 associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34<sup>+</sup> hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the  
10 immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by a  
15 subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International  
20 Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are  
25 other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL  
30 clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of  $\beta_2$ -

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio of 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The  
5 tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-  
10 1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

15 The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing  
20 screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the  
25 invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies  
30 this approach, showing the use of transfected cells expressing HPVE7 peptides in a therapeutic

regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

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size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.



Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. Immunol*, 154:5637-5648 (1995). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., *J Immunol*, 19:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Fenton et al., *J. Immunother*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS, Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these  
5 prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include  
10 keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of  
15 nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and  
20 returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and  
25 targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of  
30 viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 71:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid- $\text{CaPO}_4$  precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule.

Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

When administered, the therapeutic compositions of the present invention can be

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administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

5       The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of  
10 skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue  
15 experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer  
20 associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to  
25 diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and  
30 weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100  $\mu$ g, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen or variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response.

Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants

include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986).

Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term

"pharmaceutically acceptable" means a non-toxic material that does not interfere with the



effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as

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capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono-or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

### Examples

#### **Example 1: Preparation of breast cancer cDNA expression libraries**

##### **Step 1: Purification of total RNA from tumors.**

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

##### **Step 2: Purification of mRNA.**

A Dynabeads mRNA isolation kit (Dynal, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

##### **Step 3: cDNA synthesis.**

cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

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vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTTTT-Xba I site

Step 4: Ligation into the TriplEx vector arms.

5 The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

10 Step 6: Titering and amplification of generated libraries was performed according to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene)

15 according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
20 HBR173	$1.8 \times 10^6$ pfu	Ductal Carcinoma, Grade III
HBR184	$3.5 \times 10^6$ pfu	Invasive Ductal Carcinoma, Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
25 HBR173	$2.3 \times 10^6$ pfu	Ductal Carcinoma, Grade III
HBR184	$1.1 \times 10^6$ pfu	Invasive Ductal Carcinoma, Grade II
HBR257	$2.5 \times 10^6$ pfu	Invasive Ductal Carcinoma, Grade II
HBR297	$4.0 \times 10^6$ pfu	Ductal Carcinoma, Grade II
HBR248	$1.0 \times 10^6$ pfu	Invasive Ductal Carcinoma with Vascular Permeation, Grade III

HBR271	$2.5 \times 10^6$ pfu	Medullary Carcinoma
HBR263	$10.0 \times 10^6$ pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No  
5 serum-positive clones were found by screening HBR271 library.

#### Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at  $-70^{\circ}\text{C}$  prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH  
10 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDm) and stored at  $4^{\circ}\text{C}$ . Library screening was performed as described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of  $4 \times$   
15  $10^3$  per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at  $37^{\circ}\text{C}$ . Membranes were then blocked with 5% NFDm. As an alternative to generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3'-  
20 diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson ImmunoResearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium  
25 chloride/5-bromo-4-chloro-3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of  $5 \times 10^5$  recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

### Example 3: DNA Sequencing

- 5        Phage cDNA clones were converted to pBKCMV phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer) automated DNA sequencer. The sequences of the clones were compared with sequences in
- 10    GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
15 LONY-Br-1	L34543	LONY-Br-23	AA262134, U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
20 LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
25 LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

#### Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

The mRNA expression pattern of selected cDNA clones was determined by RT-PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

#### Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 µg poly A<sup>+</sup> RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed <sup>32</sup>P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen Clone mRNA sizes

5	Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
	LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
	LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
	LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
	LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
10	LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
	LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
	LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
	LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
	LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
15	LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
	LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
	LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
	LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
	LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
20	LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
	LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

#### Example 6: Isolation of gastric and prostate clones

A stomach cancer cDNA library was established, using standard techniques, then the library  
 25 was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7  
 30 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

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by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of  $2.5 \times 10^6$ ,  $1.1 \times 10^6$ , and  $1.7 \times 10^6$  cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of human antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'-diamino benzidine tetrachloride, and 0.015%  $H_2O_2$ , in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C. The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02%  $Na_3N$ . The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five times. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to compare signals to each other. All were positive. Table 5, which follows, summarizes some of this



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work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOS:627-634 (gelsolin, zinc finger protein family, variant zinc finger motif protein goliath and homeodomain proteins), have not  
5 been identified in humans previously, although there are related molecules found in other species. Finally, with reference to Table 5, the last four moieties, i.e., prepro- $\alpha$  collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642. The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670  
10 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all  
15 gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOS:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

#### 20 **Example 7: Isolation and analysis of colon clones**

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus  
25 obtained was then purified to isolate all poly A<sup>+</sup> RNA, using commercially available products designed for this purpose.

The poly A<sup>+</sup> RNA was then converted into cDNA, and ligated into  $\lambda$ ZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples.

30 A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g., Ace et al, Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into  $\lambda$ ZAP. All libraries were amplified, prior to immunoscreening.

Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had *E. coli* Y1090 lysates coupled thereto, and then lysates from bacteriophage infected *E. coli* BNN97 lysates. Final serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of  $4 \times 10^3$  phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described *supra*. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. The positive clones were then rescreened, using allogeneic serum, following the same method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

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cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-). Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ ID NO: 544/545 (NY-CO-8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as well as other sequences identified via the preceding examples was determined. To do this, RT-PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

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nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

5 In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

10 Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA<sup>+</sup> RNA were analyzed from these samples, using random, <sup>32</sup>P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 15 68°C, for 30 minutes each time.

SEQ ID NOS:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554 (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found 20 in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

25 The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

30 It is reported above that fourteen clones reacted with subsets of serum from both normal

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and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562

5 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophilins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537  
10 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosomal protein. The molecule set forth in SEQ ID  
15 NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with  
20 *Drosophila* homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ  
25 ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ  
30 ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

5	SEQ ID NO:	Normal Sera Reactivity	Tumor Sera Reactivity
	580	2/16	2/16
	582	2/16	3/16
10	584	2/16	2/16
	586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

15

Table 8: RT-PCR analysis of colon SEREX clones

	<u>normal tissue</u>	<u>SEQ ID NO.:550</u>	<u>SEQ ID NO.:552</u>	<u>SEQ ID NO.:558</u>	<u>SEQ ID NO.:560</u>
20	kidney	+	Negative	Negative	Negative
	colon	+	Negative	Negative	Negative
	small		Negative	Negative	Negative
	intest.	+	Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
25	stomach	+	Negative	Negative	Negative
	testis	+	Negative	Negative	Negative
	pancreas	+	Negative	Negative	Negative
	lung	+	Negative	Negative	Negative
	liver	+	Negative	Negative	Negative
30	heart	+	Negative	Negative	Negative
	fetal		Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
	mammary		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
35	bladder	+	Negative	Negative	Negative
	adrenal		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
	uterus	Negative	Negative	Negative	Negative
	skeletal		Negative	Negative	Negative
40	muscle	Negative	Negative	Negative	Negative
	PBL	Negative	Negative	Negative	Negative
	placenta	Negative	Negative	Negative	Negative

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	spleen	Negative	Negative	Negative	Negative
	thymus	Negative	Negative	Negative	Negative
	esophagus	Negative	Negative	Negative	Negative
	<u>Tumor Tissue</u>				
5	renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
	colon primary tumors (10)	+ (10/10)	+ (10/10)	+ (10/10)	Negative
10	colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
	breast cancer (6)	+ (3/6)	Negative	Negative	Negative
	lung cancer (6)	+ (6/6)	Negative	Negative	Negative
15	gastric cancer (1)	+	+	+	Not tested
	<u>colon cancer cell lines</u>				
	colo 205	+	+	+	Negative
	HT29	+	+	Negative	Negative
20	HCT15	Negative	Negative	Negative	Negative

**Example 8: Isolation and analysis of additional clones**

For the establishment of a cDNA library from human tissue total RNA was obtained from

25 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above. The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA

30 ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into  $\lambda$ ZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library

35 resulted in  $1.8 \times 10^6$  recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was  $10^{11}$  plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.



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In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic  $\lambda$  phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

5 *E. coli* bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of  $OD_{600} = 1.0$ , the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

10 A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with  $10^6$   $\lambda$ ZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

15 To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in  
20 accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of  $4-5 \times 10^3$  plaque forming units (pfu) per plate in LB-medium with  
25 isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk  
30 power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made it possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of  $1.8 \times 10^6$  recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by *in vivo* excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the  $\lambda$ ZAPII phage vectors and used for the transfection of *E. coli* SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J. *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad. Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as clone HOM-RCC-313). The Northern blot analysis demonstrated that the mRNA of clone HOM-

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RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above,  
5 allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum  
10 which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive  
15 antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme *EcoR*I, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the  
20 bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into *E. coli* of strain BL21 as described (Spindler et al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by  
25 subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with *E. coli* and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum.  
30 Reactivity was detected at dilutions of 1: >100,000.

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Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of  $8 \times 10^5$  clones were screened with autologous serum, and  $4.5 \times 10^3$  clones were screened with three different allogeneic sera. Twenty three clones, representing seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocellular carcinoma libraries were studied in the same way, a total of  $1.5 \times 10^6$  clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galectin-9 was expressed only in a small, subpopulation of dendritic cells.

Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

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above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microtubules. It was found that both restin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microtubule systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 or 5 meningioma tumor samples were found to express the gene.

#### **Example 2: Isolation and analysis of lung cancer clones**

A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a  $\lambda$ ZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci USA* 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc  $\gamma$  secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

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immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an  $^{32}\text{P}$ -labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5' end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Dracopoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5  $\mu\text{l}$  RT product in a final volume of 25  $\mu\text{l}$ , with 2  $\mu\text{Ci}$  of  $\alpha^{32}\text{P}$ -dCTP (~3000 Ci/mmol, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1  $\mu\text{l}$  of the mixture was diluted with 5  $\mu\text{l}$  of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

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denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

#### 5 Identification of Immunoreactive cDNA clones

A cDNA expression library of  $1.42 \times 10^7$  primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and  $8 \times 10^5$  phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A. Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-binding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpolished). Ubiquitously expressed.
NY-LU-3	Annexin IX [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin IX are found in multiple autoimmune diseases. ubiquitously expressed.

NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retin, multiple sclerosis, etc.
NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding arsA component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.



et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identity with reported expressed sequence tags (EST), likely representing cDNA products derived from the same genes. These ESTs were derived from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

NY-LU-12 is on TSG locus of chromosome 3p21.

The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the TSG locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res.* 56: 2487-92 (1996)]). Our analysis of LUCA15 revealed the presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies. The predominant cDNA form (SEQ ID No:707), excluding the poly A tail, is of 3591bp in length.

5 An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

Comparison with the g16 sequence verified that these two are identical genes and mapped NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the  
10 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the  
15 two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the  
20 longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

#### Additional cDNA variants of NY-LU-12

25 In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

30 Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

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nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D). Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

#### Features of NY-LU-12 and its putative gene product

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs, rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

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et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3' end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

#### Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), Lu15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition.

This possibility was explored using DNA sequencing and single-strand confirmational polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous normal lung tissue, and no mutations were found when compared to Lu15-251.

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of SSCP analysis is shown in Fig. 5.

Serological response to NY-LU-12 in lung cancer patient

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

Example 10: Expression analysis of additional cancer associated nucleic acids

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only in testis, which was then investigated by RT-PCR analysis as described above.

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The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone 1 Testis; GenBank accession number M60094) was

5 identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

H1R1: GCTTCGTGTAGATTTAGGAATC (bp 344-366 of H1T)

10 Table 10: RT-PCR analysis

	<u>Normal Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	mammary gland	-	-
	liver	-	-
15	small intestine	-	-
	brain	-	+/- (very weak)
	lung	-	-
	fetal brain	-	-
	placenta	+	+
20	kidney	-	-
	skeletal muscle	-	-
	pancreas	-	-
	adrenal gland	-	-
	heart	-	-
25	thymus	-	-
	uterus	-	-
	prostate	-	+/- (very weak)
	spleen	-	-
	Testis	+	+

30

	<u>Tumor Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	Colon	0/6	0/6
35	Breast	0/6	6/6+
	Melanoma	0/12	3/12+
	Lung	8/26+	4/26+
	Renal	0/2	0/2
	Ovary	0/2	0/2
40	Esophageal	0/1	0/1

Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was expressed only in normal testis and possibly in placenta. The expression analysis of H1T revealed that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples expressed H1T. H1T was expressed in normal testis and possibly in placenta and brain.

#### **Example 11: allogeneic serotyping**

To confirm the cancer associated expression of SEREX clones, allogenic sera screening of gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a control for expression of the clones in non-gastric cancer. The screening procedure used was as described above for the SEREX screening, except for the absorption of anti-bacterial and anti-bacteriophage antibodies. The modifications were as follows.

Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep Chromatography Column, Hercules, CA, USA) containing 0.5 ml Sepharose-4B cross linked to E. coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc, Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and bacteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic typing, an equal numbers of positive phage and negative phage were mixed and plated and processed by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

**Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients**

Sequence		Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
Gene/Clone	Number			
5 RPB-J H-2K binding factor		SM1	6/12	6/16
Telomeric repeat binding protein		SM1	1/12	0/16
Ser/Thr protein kinase		SM1	1/12	0/16
SRY interacting protein-1		SM1	2/12	1/16
Sterol carrier protein X		SM1	2/12	0/16
10 Archain		SM1	1/12	1/16
HEM-1		SM1	2/12	1/16
Id-1 helix-loop-helix protein		SM1	1/12	0/16
15 helix-loop-helix transcription factor		SM1	1/12	0/16
Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
20 M phase phosphoprotein I		SM1,SS1	8/12	5/16
Lysal tRNA synthase		SM1	1/12	0/16
Gelsolin		SM1	4/12	0/16
Zinc finger protein		SM1	1/12	1/16
Goliath		SM1	2/12	1/16
25 zhx-1		SM1	1/12	1/16
SG24		SM1,SS1, KM	5/12	0/16
SG132		SM1	3/12	0/16
S553		SM1	7/12	7/16
S134		SM1	3/12	0/16
30 S328		SM1	2/12	1/16
S365		SM1, KM	2/12	0/16



	FKBP25		KM, SS1	5/12	0/16
	Pros-27		KM, CK	3/12	1/16
	BS4		KM	1/12	1/16
	GnRH-II		KM	1/12	0/16
5	CTBP		KM	1/12	0/16
	ETF		KM	3/12	1/16
	KIAA0438		KM	1/12	5/16
	KIAA0367		KM	4/12	3/16
	APK1		KM	2/12	0/16
10	IPP		KM	1/12	0/16
	Tropomyosin		KM	1/12	0/16
	p63		KM	1/12	0/16
	KIAA0181		KM	1/12	0/16
	KIAA0349		KM	1/12	0/16
15	RPB1		KM	5/12	9/15
	PPIM		KM	1/12	-
	EB virus		KM	3/12	-
	G.KM073		KM	6/12	-
	G.KM403		KM	1/12	-
20	KM192		KM	1/12	-
	KM294		KM	1/12	-
	KM362		KM	1/12	-
	KM031		KM	1/12	-
	KM081		KM	3/12	-
25	KM201		KM	1/12	-
	KM1496		KM	1/12	-
	KM334		KM	1/12	-
	KM313		KM	1/12	-
	E-cad/Y		CK	1/12	0/16
30	IPBP		SS1	1/4	-
	OS-9		SS1	1/4	-

Kinesin light chain	...	SS1	1/4	-
---------------------	-----	-----	-----	---

The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, 5 follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

#### 10 **Example 12: Preparation of recombinant cancer associated antigens**

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into 15 appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated 20 the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression 25 systems and mammalian cell culture systems also can be used.

#### **Example 13: Preparation of antibodies to cancer associated antigens**

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The 30 antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

**Example 14: Expression of cancer associated antigens in cancers of similar and different origin.**

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

**Example 15: HLA typing of patients positive for cancer associated antigen**

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

5

**Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.**

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in

15 Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (see, e.g., Parker et al, *J. Immunol.* 152:163, 1994; D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpennig (PCT/US96/03182)).

20

The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

25

30 Table 12: Identification of HLA binding peptides in lung SEREX clones

- 85 -

		amino acids of		
HLA	peptide	NY-LU-12 protein	SEQ ID NO	
5	A1	NVEE-HSFSY	67 - 75	713
		PVDP-NILDY	287 - 295	714
		DTDY-RSMEY	398 - 406	715
10	A2	SLLE-DAIGC	506 - 514	716
		TLMI-QDKEV	521 - 529	717
		YVSSLDFWYC	533 - 542	718
		VIVEVLEPYV	671 - 680	719
		KLTD-WNKLA	948 - 956	720
		QLSDLHKQNL	975 - 984	721
		KQSEQELAYL	991 - 1000	722
		KLVDKEDIDT	1042 - 1051	723
15		VMFA-RYKEL	1114 - 1122	724
20	A3	QMFG-YGQSK	417 - 425	725
		GMPVKNLQLK	481 - 490	726
		GLPE-EEEIK	823 - 831	727
		LLCRRQFPNK	958 - 967	728
25	A24	EYRD-VDHRL	405 - 413	729
		GYVC-VEFSL	499 - 507	730
		DYGY-VCVEF	497 - 505	731
		WYCKRCKANI	540 - 549	732
		TYPQPQKTSI	574 - 583	733
		IYRSTPPEVI	663 - 672	734
		HYYQ-GKKYF	754 - 762	735
		VYVP-QDPGL	816 - 824	736
30	B7	WNRDYPPPPL	26 - 35	737
		MPPV-DPNIL	285 - 293	738
		TARD-AQRDL	432 - 440	739
		GPSEEKPSRL	448 - 457	740
35		TPPEVIVEVL	667 - 676	741
		RVMFARYKEL	1113 - 1122	742
40	B44	REMG-SCMEF	272 - 280	743
		EEQSSDAGLF	376 - 385	744
		KEYN-TGYDY	490 - 498	745
		TEAKQELITY	566 - 575	746
		VEALRVVKIL	710 - 719	747
		GEYG-GDSY	906 - 914	748
		LERREREGKF	1000 - 1009	749

- 86 -

5	B52	RQDGESKTIM	650 - 659	750
		TPPEVIVEVL	667 - 676	751
		YGFIDLDSHV	701 - 710	752
		RQFP-NKEVL	962 - 970	753
NY-LU-12B (variant B)				
10	A1	NVEE-HSFSY	121 - 129	754
		PVDP-NILDY	341 - 349	755
		DTDY-RSMEY	452 - 460	756
15	A2	WQSA-RFYYL	41 - 49	757
		SLLE-DAIGC	560 - 568	758
		TLMI-QDKEV	575 - 583	759
		YVSSLD FWYC	587 - 596	760
		VIVEVLEPYV	725 - 734	761
		KLTD-WNKLA	1002 - 1010	762
		QLSDLHKQNL	1029 - 1038	763
20		KQSEQELAYL	1045 - 1054	764
		KLVDKEDIDT	1096 - 1105	765
		VMFA-RYKEL	1168 - 1176	766
25	A3	QMFG-YGQSK	471 - 479	767
		GMPVKNLQLK	535 - 544	768
		GLPE-EEEIK	877 - 885	769
		LLCRRQFPNK	1012 - 1021	770
30	A24	YYLN-ATDVL	47 - 55	771
		FYYLNATDVL	46 - 55	772
		EYRD-VDHRL	459 - 467	773
		GYVC-VEFSL	553 - 561	774
		DYGY-VCVEF	551 - 559	775
		WYCKRCKANI	594 - 603	776
35		TYPQPQKTSI	628 - 637	777
		IYRSTPPEVI	717 - 726	778
		HYYQ-GKKYF	808 - 816	779
		VYVP-QDPGL	870 - 878	780
40	B7	WNRDYPPPPL	80 - 89	781
		MPPV-DPNIL	339 - 347	782
		TARD-AQRDL	486 - 494	783
		GPSEEKPSRL	502 - 511	784
		TPPEVIVEVL	721 - 730	785
45		RVMFARYKEL	1167 - 1176	786

- 87 -

5	B44	SEAWSSNEKF	59 - 68	787
		REMG-SCMEF	326 - 334	788
		EEQSSDAGLF	430 - 439	789
		KEYN-TGYDY	544 - 552	790
		TEAKQELITY	620 - 629	791
		VEALRVVKIL	764 - 773	792
		GEYG-GDSY	960 - 968	793
		LERREREGKF	1054 - 1063	794
10	B52	RQDGESKTIM	704 - 713	795
		TPPEVIVEVL	721 - 730	796
		YGFIDLDHV	755 - 764	797
		RQFP-NKEVL	1016 - 1024	798

15 Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

**Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen**

20 To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching

25 the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see, e.g., Knuth et al., Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230,

30 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by <sup>51</sup>Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or  $^{51}\text{Cr}$  release as above.

5 Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

10 A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

#### 15 EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

20 All references disclosed herein are incorporated by reference in their entirety.

We claim:



## TABLE 1

## SEQ ID NO. 1:

- 5 U72994, AC004022, Z68323, AE001160, L34078, AF064863, AC002132, U60440, X66494, N21242, AA678312, W86762, R01605, AA782843, AA275156, W41927, AA874648, AA571241, AA562747, W10480, AA451301, AA866631, AA466667, AA999057, AI029140.

## 10 SEQ ID NO. 2:

AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648, AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648.

15

## SEQ ID NO. 3:

- X98371, AL009008, L31790, Z83220, X92946, AC003975, AF008916, U80460, X75544, X66732, X95275, X52177, X07976, AC004451, Z74307, AB000878, AL009179, AF038667, 20 Z78544, Z48008, U23486, J05096, AB000882, Z30213, L11593, U18530, L27325, AC005191, M99579, AA130270, AA158245, AA903098, AI018453, AA436455, AA980593, AA172479, AA637487, AA116588, AA426854, AA050404, AA390025, AI006618, AI048382, C85944, AA673480, AI006510, AA823338, AA413694, W35075, AA015033, AA413584, W29693, AA637069, AA619839, AA125149, AA039004, AA674696, AA871138, AA414747, 25 AA198099, C91478, F071359, AA925957, AA820054, H16496, AI043756, AA892435, AA893551, AA818669, AA892785, AA944026, D33919, N96570, F19798, AI045451, AA800662, D65187, AA944025, AA925731, AA892314, AA945449.

## 30 SEQ ID NO. 4:

AA900930, AA925665.

## 35 SEQ ID NO. 5:

- U58105, Z81485, Z54236, Z48584, U61375, M55267, M59856, X51942, U77302, Z48621, AF032455, Z11866, AB013392, L32792, AA871997, AA084083, AA130829, AA083063, AA666290, N38894, D54459, T28921, AA806015, AA512059, AI043087, AI042894, 40 AA968324, AA238493, AA237462, AI042885, AI046424, AI035670, AA269430, AA250621, AI035540, AA260613, AA106870, AA238658, AA106134, AI042683, AA105958, AA144007, AA986558, AA457910, AA389400, AA673056, AA153254, AA754678, AI021109, AA390813, C36687, T41571, AI011183, AI013356, AI011739, AI030260, AA924384, C44421.

45

## SEQ ID NO. 6:

AF036717, U91327, AF036718, U56248, Z48795, Z99290, M30697, U58204, M24417, AF022983, M33581, AC004619, H64641, AA477478, AA369676, AA088359, AA057574,

AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527,  
AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204,  
AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395,  
AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787,  
5 AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

## SEQ ID NO. 7:

10 X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750,  
X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008,  
D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337,  
X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880,  
AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916,  
15 AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461,  
AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410,  
AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615,  
AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

20

## SEQ ID NO. 8:

U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506,  
M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054,  
25 AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309,  
AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611,  
AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258,  
AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075,  
N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161,  
30 AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148,  
AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792,  
AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516,  
AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779,  
AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483,  
35 C64685, AA851367, C91730, AA143899, T23399.

## SEQ ID NO. 9:

40 AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241,  
AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846,  
AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802,  
AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761,  
C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390,  
45 AA848674, AA924440, T15031, AA451569, H35524.

## SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

5

SEQ ID NO. 11:

AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647, 10 AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274, 15 AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, AI75818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956, 20 AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

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SEQ ID NO. 13:

X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051, 40 X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713, 45 H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

## SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619,  
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## 10 SEQ ID NO. 15:

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15 AA620556, AA085733, AA187157, AI031865, AA972318, AA897169, W79046, AA531124,  
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## SEQ ID NO. 16:

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## 40 SEQ ID NO. 17:

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45 AB011800, M77194, AE000021, L07268, AE000936, U03115, AF009663, AA582128,  
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- AA320235, AA864472, T16369, AA588049, AA399159, AA148239, AA143432, AA962682, AA062646, AA335060, AA579762, R10999, AA858417, AA603170, AA292786, AA374867, AA191035, AA191500, AA599385, AA190396, T96301, AA535568, AA857439, AA977124, AA159515, AA719754, R61295, AA079690, AA577057, AA171709, AA552769, AA456451, 5 N26291, AA132216, AA070196, H45529, AA160327, AA970357, AA477493, AA421297, AA017413, AA857677, T51717, AA081099, AA977849, N80148, AA335988, AA908779, AA377875, AA385959, R60668, AA335517, AA074035, N74403, N74349, AA573544, W86143, AA001378, R20658, AI025133, AA292257, AA421421, H56664, N39032, AA641715, AA020820, , AI047425, AA472466, AA590221, C79020, AA212086, AA071597, 10 AA106338, W08130, W97930, AA592853, AA231046, W64197, C79418, AA823938, AA221509, C79656, AA245954, AA682101, AA855850, AA473492, W08536, AA260905, AI049102, AA185645, W89717, AA109639, AA733290, W33785, C76616, AA733222, AA519045, W34372, AA066569, AA691645, AA572427, C79871, AA255234, W63015, AA689692, AA688470, AA066196, AA403359, AA210393, C81440, W82152, AA563263, 15 AA096538, AA008688, AA412918, AA674747, AA214774, AA823987, AA896527, AA756088, AA538420, AA124828, AA067750, AA671458, AA792196, AA855848, W14531, AA432423, AA562178, AA207523, C77610, AA073011, AA060218, AA691391, AA103515, AA245550, AA222057, C78107, AA608092, AA104942, AA408984, AA855192, AA144906, AA895345, AA796175, W41390, AA387888, C77993, AA144316, AA716803, AA276281, 20 AA396852, AA637534, AA107667, AA119982, W09492, W09768, AA771341, AA144901, AA880477, C79311, AA717872, AA272656, C88492, C81442, AA981878, AA606217, AA605671, AA605977, AA605664, AA894180, AI008538, AI012445, AA945532, AA945028, AA012736, AA850423, AA891167, AA851948, AA964432, AA753449, AA542773, AI008780, AA022374, L38072, AA169924, T00115, T00217, F23046, F15046, C07018, T00696, 25 AA753701, T00169, C07195, AA750404, W51726, C07173, AA109326, AA753730, AA109292, AA169908, W51717, AA675873, AA751451, F15031, AA842359, W91870, R95270, AA754092, AA751719, AA751718, AA509249, AA753934, AA952484, AA962878, AA751728, AA752131, AA754188, F13957, T41487, AA433419, AA471455, AA471706, AA754093, N60029, AA406919, D67349, AA754187, T41457, R88411, AA406840, 30 AA417423, AA470325, AA680491, AA754048, Z92686, T44319.

## SEQ ID NO. 18:

- 35 U14003, AE000500, X66784, AF030178, U77066, M10122, M69106, X58072, Z99113, AF004104, AF004101, X55037, X78560, AC004595, X55122, AA481578, AA280143, AA481271, AA280144, AA736516, N79995, R82883, AA355987, AA571000, AA572293, AA738653, AA620225, AA855746, AA563168, AA530645, W40812, AA690944, AA839456, X61848, AA525648, AA141861, AA944854, C94212, AA394778, C83861, H76642, 40 AA559379, AA943112.

## SEQ ID NO. 19:

- 45 AE000500, AF030178, X66784, Z49405, M69106, M27174, X55037, AF004104, X78560, U51281, L17405, M10122, AC003106, X55122, X05553, AC002368, AF004101, U77066, U77456, X58072, AA481578, AA280143, AA481271, AA280144, AA736516, AA780050, AA359089, R82883, AA355987, AA571000, AA563168, AA738653, AA620225, AA855746, AA572293, AA530645, W40812, AA690944, AA839456, X61848, AA525648, AA944854,

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SEQ ID NO. 20:

5 Z99496, AC004518, AC004219, Z70204, J03925, Z66494, AC003053, U40072, AC002980,  
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10 AA874804.

SEQ ID NO. 21:

15 U20864, AL021246, AA430998, AA050776, AA104086, AA414390, AA920944, AA624117,  
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SEQ ID NO. 22:

20 Z81462, AF029308, AC004069, AL010265, AL023828, AC004026, AF076274, U96110,  
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SEQ ID NO. 23:

30 X60469, AC000394, L08048, X12597, D63874, U51677, S71186, D43920, U59897, AF026132,  
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35 AF039845, L06147, M60052, X56007, Y00500, X77934, U26708, AL022333, AL021710,  
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40 L06098, L19713, U88047, S67316, U47276, U28389, U18650, M85183, U07886, U00762,  
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25 D48397, D72544, D72553, AA963561, M89319, D24210, D23745, D72761, C59680,  
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## SEQ ID NO. 24:

30 Z93928, U13881, U70475, X89811, X81456, U20532, X04724, J00748, M25585, J04807,  
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35 C01240, W65459, AA416662, N48671, AA759070, N29058, H06159, R97183, F20369,  
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40 AA498683, AI046409, C85159, Z84147, AA893230, C06683, C06682, C06639, C06625,  
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## SEQ ID NO. 25:

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## SEQ ID NO. 26:

15 D38548, M59201, U67559, L29453, L27707, X52142, M58326, U49350, AL021806,  
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AA515984, AA962233, AA332628, W90207, W55983, R98570, AA937512, AA190722,  
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25 S87757, AJ005457, J04503, D28117, AL009051, AL022603, M86359, Z84489, AA625572,  
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30 AA497692, AA855719, C85235, AA407160, AA516930, AA240636, W41595, AA475660,  
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## 35 SEQ ID NO. 28:

Z84812, X56744, AB007445, AE000947, AF038854, X98801, AB013487, U40575, AF002992,  
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45 AI021096, AA275231, AA433044, AA221284, AA822351, AA014416, AA986428, AA221500,  
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5 SEQ ID NO. 29:

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SEQ ID NO. 30:

25 AL022394, Z54200, U12024, AF025391, S73606, L08068, U01053, AP000046, AA282633, H83341, AA744757, AA047741, AA975917, W45279, W90155, W79733, H01158, N47513, AA688093, AA865203, W90027, AA595381, AA054203, AA478596, AA100549, T80668, AI049820, AA047691, AA969720, AA086374, AA159414, W39756, AA159315, H83695, 30 AA909221, T06258, AA969838, AA013361, H05751, H05858, AA665540, D12197, H01159, AA933811, D12219, AA282525, C05204, N47512, R57383, F18424, D79284, W92778, H18813, H20386, N77238, R84635, AA204675, R80129, W95005, T85150, AA523436, AA743656, T84782, W95004, R55724, AA572180, AA790119, W96964, AA420091, AA169954, AA623914, AA623971, AA681631, H32698, AA735717, AF026318.

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SEQ ID NO. 31:

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## SEQ ID NO. 32:

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## SEQ ID NO. 33:

10 U10079, U22176, Z97192, X86553, D16432, Z68908, X98417, X97752, AC005176,  
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## 20 SEQ ID NO. 34:

AF041845, U48436, AF012624, L76569, AF025020, AF060179, U51281, Z37092, L12249,  
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## SEQ ID NO. 35:

30 AF069301, D17030, D17201, S80107, M15888, U09205, J00127, J00128, M64982, L11356,  
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35 AA103723, AA800548, T46478, AA751512, C10724, C60506, AA819627.

## SEQ ID NO. 36:

40 U81160, U35246, U66865, AF036234, Z71178, R52780, AA336715, AA337057, R12336,  
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## SEQ ID NO. 38:

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## SEQ ID NO. 39:

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## SEQ ID NO. 40:

25 AB002307, X06289, Y00222, U59322, U28964, X61754, AJ004801, U13913, X79339, AA164880, R02386, AA219744, AA324396, D82199, AA113090, AA305260, AA171458, R59748, R35620, AA326344, AA227875, AA366276, H29212, AA505691, R78747, AA406622, AA020232, W64555, AA450476, W44167, AA049918, W64627, R75474, 30 AA517492, AA612452, AA711884, AA212469, AI048148, AI046831, AA671392, AA855606, AA016843, AA031134, AA208052, AA619148, W34918, AA851114, AA901667, AA054812, AI001233, AA955131, AA943821, AI008608, C72506, AI001373, AI001376, D25096, D21962, AA997901, AA824936, AA998885, AA824820, AA998125, AA859586.

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## SEQ ID NO. 89:

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SEQ ID NO. 91:

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30 SEQ ID NO. 93:

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SEQ ID NO. 115:

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SEQ ID NO. 119:

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SEQ ID NO. 131:

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SEQ ID NO. 133:

U48587, U68267, AF001906, AF033856, M33336, U73177, J03685, AC004743, AC004539, Z60442, N53159, N75331, AI042621, AA435593, AA608757, AA076290, AA662552, AA213762, AA630025, R57980, N24985, AA813323, H21646, H05642, AA359799, AA191039, AA318867, H15234, AA323419, N27160, AA636826, AA656934, AA726211, 5 AA619507, AA792581, W59642, AA035921, AA637995, AA667370, AA592134, AA637894, AA591158, AA756070, AA467467, AA739462, AA272875, AA214985, AA739083, AA914526, AA386742, AA919409, AI046649, W35790, AA016357, W97992, AA656026, AA414710, AI006426, AA673795, AA239695, AA285593, AA615757, AA038932, AA073580, AA103792, AA220731, C85146, AA867112, AA028705, AA118743, AI005830, 10 AA874206, AA451006, AA667719, AA637623, AA492608, AI048487, AA189854, AA116581, AA096759, R04321, R04399, Z48427, R04620, R04065, R04404, R04422, R03209, C51162, C44210, R05229, C49234, R03208, R04273, D75630, D75447, D75141, D74833, D74636, D74299, D70237, R05254, C42102, AA658642, AA685519, AA799735, C93660, AA685980, AA750619.

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SEQ ID NO. 135:

AC005175, L12168, M98474, U94696, M88485, Z95972, Z81557, S54909, U59831, 20 AB002387, U59832, AC004221, AC003993, AA505656, AI004052, AA975150, AA904315, R39951, AA908198, AA348001, AA348002, R39437, R39435, D21034, AA365146, AA813999, F12674, AA226122, T50818, AA143492, AA337395, AA003016, AA475640, W78672, AA517530, W45934, AA915424, W54264, AA168145, W11712, D34652, U92753, Z84127, U92730, AA438286, AA978864, AA941236, F14527, D47303, D15953, AA202003, 25 AA979012, AA440964, AA736036, AA246888, AA940864.

SEQ ID NO. 137:

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SEQ ID NO. 139:

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M24603, X02596, Y00661, M15025, X06418, U07000, X52829, M19730, M30829, X52831, M30832, X14676, X52828, X52830, S72479, L02935, M64437, M17542, L19704, U01147, X07537, X14677, X14675, M17541, M17543, M19695, X76485, AF023460, X89600, U19759, AF039083, X71790, AC004679, AC002076, AF035456, M99565, Z72005, Z79997, AL021154, 45 Z98259, AC003108, L13706, AF018254, M69197, U67228, Z75887, U14661, M84472, AC005200, AC001228, AC004761, Z95124, AC002540, Z79699, AE000926, U43572, U51281, D82351, AB013379, U34879, AC002425, AC004598, AA338585, AA333142, AA126116, H55543, H55721, R54267, H55614, H55699, H55545, AA744741, AA772917, H29052, AA573543, T16608, AA773472, AA775416, AA601919, AA470534, AA351521,

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SEQ ID NO. 141:

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S45630, AF007162, X95383, AF029793, M55534, X60351, S77138, S77142, S74229, X60352,  
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S53164, U26661, M12015, M25770, U16124, X87114, D29960, X14789, X85205, M17247,  
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AA482745, AA211607, N28898.

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SEQ ID NO. 143:

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35

U78082, L78810, U14573, AC004068, U07561, M98511, AC004673, AA613346, AA953216,  
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AA663472, AA490602, AA857673, AA347114, AI049630, AA086150, AI017251, AA877992,  
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SEQ ID NO. 145:

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45

SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873,  
L07874.

SEQ ID NO. 149:

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5 AA732931, AA610556, AA973899, AA598896, AA531553, AA826535, AI000209, AA290836,  
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AA833281, AA619252, C77541, AA691960, AA763615, AA164051, AA259589, AA060475,  
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10  
SEQ ID NO. 151:

M13451, X03445, X03444, M13452, X66870, X76297, X14170, X99257, D14850, D13181,  
L12399.

15  
SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

20  
SEQ ID NO. 155:

X54859, Z86000, AC003043, X77738, X77737, L35930, AC003084, AC000111, M89651,  
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AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892,  
35 C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855,  
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40  
SEQ ID NO. 157:

U43195, U58512, U61266, D89493, U36909.

45  
SEQ ID NO. 159:

AF069442, AF001295, M13820, M10081, AB010077, AA491075, AA446881, AA588390,  
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AA882303, AA791693, AA822133, AI037224, AA404165, AI036575, AA499662, AA864136,  
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02866, H35041, AA944944, AA597316, D26977, D68334, AA685934, W88345, AA964819.

## SEQ ID NO. 161:

5 K01546, AE000468, X95549, AC004014, Z81584, L19201, X94244, X06932, U39479,  
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10 AA397279, AA420226, AA396042, AA200070, AA165873, AA762534, AA067133,  
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## SEQ ID NO. 163:

20 X15183, AF028832, D87666, J04633, L33676, X07270, U94395, M27024, M30627, X16857,  
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30 AA657352, AA522607, AA188113, AA026444, AI003623, AA312717, AA312400, T64299,  
AA178992, AA228992, AI042136, AA457613, AI032857, AA164461, AA625127, AA807763,  
AA130815, AA054695, AA937097, W93534, N67875, AA526896, W52802, AA527942,  
N34251, W28646, AA668543, AA496091, W52511, AA070581, AA306826, AA120908,  
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35 AA225404, AA127417, AA854951.

## SEQ ID NO. 165:

40 M23885, AF047868, AF017732, AB005249, Z83229, AF026483, U97194, Z67884, Z67881,  
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45 AA261777, N40306, W21253, R02386, AA349225, AI038487, H98027, AA385878,  
AA075431, AA375596, R77638, T73214, AA310841, AA062331, AA919318, AA606883, 373  
AA174568, AA790426, AA423321, AA647673, AA109549, AA396473, W16215, AA105538,  
AA061105, AA066766, AA462773, AA555644, AA499452, AA389523, AA245036,  
AA475340, AA880992, AA198965, W11981, AA509705, AA237414, AA646230, AA673569,

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SEQ ID NO. 167:

Y11251, AF030234, AF043945, L40407.

SEQ ID NO. 169:

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SEQ ID NO. 170:

D32050, D16969, AC004423, S81497.

SEQ ID NO. 172:

D86982, L07131, M14544, AA296228, AA318436, AA296234, H88394, W26642, AF038251, AA394101, N35855, N56791, N35444, AA147382, AA647547, AA939939, AA895989, AA122437, AA277698, W75741, AI036117, AA980469, AA033178, AI006694, AA980625, AA033190, AA175922, AA172918, AA895209, AA028700, AA416048, AA175247, AA217057, AI045760, R64866, D40836, D41873, AA509279, D40089, AA114361, AA751642, AA848690, AA800525, AA802510, C24001, AA841755, AA882663, D40069, AA433358, D40199, AA958134, AA072494, AI008727, AA618978, AA848687, C21884, AA113662, AA945653, AA660093, C58446, AA908068, AA532100, AA264560, AA426658, AA097169, AA751535.

SEQ ID NO. 174:

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SEQ ID NO. 176

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SEQ ID NO: 177

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SEQ ID NO: 178

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## SEQ ID NO: 179

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15 SEQ ID NO: 194

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45 SEQ ID NO: 198

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35 AA130392, AA486261, AA569324, AA503924, N57307, AI016392, AA630335, AA079126,  
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45 D75878, D76297, AA859311, F19815, C62071, C63980, AA539230, AA875056, D33778,  
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10 AA115152, R49041, F02743, AA125794, AA281970, AA639166, AA127093, AA573768,  
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F02957, AA347035, W73300, AA061413, W96984, AA530599, F14212, C22934, AA926098,  
C92915, D27726, AA924800, AA923860, C55124, AA892301, AA549967, AA751821,  
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SEQ ID NO: 261

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5 SEQ ID NO: 263

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SEQ ID NO:264

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35 SEQ ID NO:265

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SEQ ID NO: 268

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SEQ ID NO: 269

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10 AA497505, AA561627, AA959889, AA413826, AA530017, AA681704, AA718524,  
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15 SEQ ID NO: 270

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D39545.

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SEQ ID NO: 271

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## SEQ ID NO: 272

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## SEQ ID NO: 274

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## SEQ ID NO: 275

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## SEQ ID NO: 276

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## SEQ ID NO: 277

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5 SEQ ID NO: 321

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## 35 SEQ ID NO: 471

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SEQ ID NO: 472

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15 SEQ ID NO: 473

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## SEQ ID NO: 475

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30 AA931026, AA999328, AI018982, AA517952.

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20 AA198469, AA797491, AA655766, AA546928, AA510411, W42224, AA944833, AI009004,  
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40 AA494753, AA041007, C94155, F15350, AA395308, C23188, AA944028, AI029279,  
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5 AA390238, T88530, C93064, N38560, C71320, D37215, T44514, AA224662, T42682.

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D78731, AA872016, AA533831, AA486536, AA112946, AA458173, AA985699, AA438072,  
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Z26528, AA395112, AA586078, D41457, AA193962, AA915808, AA193969.

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SEQ ID NO: 486

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25 AA119459, AA999641, AA509268, AA109389, AA161638, AA508962, AA123529, C91548,  
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35 AC000118, AF047825, Z70280, AP000021, Z92844, AC004112, AF030453, M63796, U14574,  
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SEQ ID NO: 506

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20 SEQ ID NO: 507

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35 SEQ ID NO: 508

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25 SEQ ID NO: 512

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45 SEQ ID NO: 514

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 W84968, W84968 mf42e02.rl Soares mouse embryo NbME13.5 14.5 M... 640 0.0  
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 AA673899, AA673899 vo86g07.rl Barstead mouse irradiated colon... 583 e-164  
 AA797488, AA797488 vw28a05.rl Soares mouse mammary gland NbMM... 519 e-145  
 W71831, W71831 me45b06.rl Soares mouse embryo NbME13.5 14.5 M... 472 e-131  
 AA213358, AA213358 mu74e04.rl Stratagene mouse embryonic carc... 444 e-123  
 W75918, W75918 me82f05.rl Soares mouse embryo NbME13.5 14.5 M... 444 e-123  
 AA038141, AA038141 mi81e05.rl Soares mouse p3NMF19.5 Mus musc... 359 3e-97  
 AA038288, AA038288 mi83b04.rl Soares mouse p3NMF19.5 Mus musc... 323 1e-86  
 AA017742, AA017742 mh40c03.rl Soares mouse placenta 4NbMP13.5... 297 8e-79  
 AA771297, AA771297 vt17g04.rl Barstead mouse myotubes MPLRB5 ... 297 8e-79  
 AA105228, AA105228 mp45b11.rl Barstead MPLRB1 Mus musculus cD... 295 3e-78  
 AA068340, AA068340 mm53f01.rl Stratagene mouse embryonic carc... 293 1e-77  
 AA612347, AA612347 vo05c08.rl Stratagene mouse skin (#937313)... 281 5e-74  
 AA038300, AA038300 mi83d04.rl Soares mouse p3NMF19.5 Mus musc... 270 2e-70  
 AA500952, AA500952 vg01h04.rl Soares mouse NbMH Mus musculus ... 252 4e-65  
 W08368, W08368 mb41f07.rl Soares mouse p3NMF19.5 Mus musculus... 212 4e-53  
 AA052280, AA052280 ma82e12.rl Soares mouse p3NMF19.5 Mus musc... 123 3e-26  
 AA064466, AA064466 ml49c05.rl Stratagene mouse testis (#93730... 107 2e-21  
 AA271566, AA271566 vb74b09.rl Soares mouse 3NME12 5 Mus muscu... 60 3e-07  
 C86222, C86222 Mus musculus fertilized egg cDNA 3'-end seque... 42 0.078  
 W83632, W83632 mf31a04.rl Soares mouse embryo NbME13.5 14.5 M... 42 0.078  
 AA423627, AA423627 ve80f01.rl Soares mouse mammary gland NbMM... 42 0.078  
 AA036586, AA036586 mi41h08.rl Soares mouse embryo NbME13.5 14... 42 0.078  
 AA207496, AA207496 mv78g02.rl GuayWoodford Beier mouse kidney... 42 0.078  
 AA120433, AA120433 mp82h11.rl Soares 2NbMT Mus musculus cDNA ... 42 0.078  
 W08185, W08185 mb42h02.rl Soares mouse p3NMF19.5 Mus musculus... 38 1.2  
 AA065563, AA065563 ml71b06.rl Stratagene mouse kidney (#93731... 38 1.2  
 AA288756, AA288756 mr46h07.rl Life Tech mouse embryo 15 5dpc ... 38 1.2  
 AA119334, AA119334 mp80e10.rl Soares 2NbMT Mus musculus cDNA ... 38 1.2  
 AA163051, AA163051 ms24a10.rl Stratagene mouse skin (#937313)... 38 1.2  
 N28074, N28074 MDB1392R Mouse brain, Stratagene Mus musculus ... 38 1.2  
 AA288757, AA288757 mr46h08.rl Life Tech mouse embryo 15 5dpc ... 38 1.2  
 AA122857, AA122857 mq06a02.rl Soares 2NbMT Mus musculus cDNA ... 38 1.2  
 AA617519, AA617519 vj77d05.rl Knowles Solter mouse blastocyst... 38 1.2

W89420, W89420 mf80b03.rl Soares mouse embryo NbME13.5 14.5 M... 38 1.2  
 AI047837, AI047837 ud64c11.xl Sugano mouse liver mlia Mus mus... 38 1.2  
 AA840310, AA840310 vw91a10.rl Stratagene mouse skin (#937313)... 36 4.8  
 AA986428, AA986428 ue13b04.xl Sugano mouse embryo mewa Mus mu... 36 4.8  
 W47677, W47677 mc89g07.rl Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA057996, AA057996 mj56c10.rl Soares mouse embryo NbME13.5 14... 36 4.8  
 AA183858, AA183858 mo95h01.rl Stratagene mouse testis (#93730... 36 4.8  
 AA212232, AA212232 mu43e08.rl Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 W41067, W41067 mc39a06.rl Soares mouse p3NMF19.5 Mus musculus... 36 4.8  
 AA967594, AA967594 uh01d06.rl Soares mouse hypothalamus NMHy ... 36 4.8  
 AA414093, AA414093 vc64c07.sl Knowles Solter mouse 2 cell Mus... 36 4.8  
 AA123833, AA123833 mp93c03.rl Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 AA432920, AA432920 vd91b11.rl Soares mouse NbMH Mus musculus ... 36 4.8  
 AA874496, AA874496 vx03a08.rl Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 AA000433, AA000433 me76e09.rl Soares mouse embryo NbME13.5 14... 36 4.8  
 AA023983, AA023983 mh94a07.rl Soares mouse placenta 4NbMP13.5... 36 4.8  
 AA013726, AA013726 mh12e09.rl Soares mouse placenta 4NbMP13.5... 36 4.8  
 AA274648, AA274648 vb08c01.rl Soares mouse NML Mus musculus c... 36 4.8  
 AA140347, AA140347 mq89g06.rl Stratagene mouse heart (#937316... 36 4.8  
 AA499377, AA499377 vi89c07.rl Stratagene mouse heart (#937316... 36 4.8  
 C88747, C88747 Mus musculus early blastocyst cDNA, clone 01B... 36 4.8  
 AA726125, AA726125 vu88c06.rl Stratagene mouse skin (#937313)... 36 4.8  
 AA760311, AA760311 vv71c12.rl Stratagene mouse skin (#937313)... 36 4.8  
 AA763007, AA763007 vw60b05.rl Soares mouse mammary gland NMLM... 36 4.8  
 AA929878, AA929878 vz44d03.rl Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 W59064, W59064 md67e10.rl Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA103519, AA103519 mo24b12.rl Life Tech mouse embryo 13 5dpc ... 36 4.8  
 AA222310, AA222310 my14d08.rl Barstead mouse heart MPLRB3 Mus... 36 4.8  
 W83557, W83557 mf32d02.rl Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA168631, AA168631 ms33c05.rl Stratagene mouse skin (#937313)... 36 4.8  
 AA960143, AA960143 vw60b05.sl Soares mouse mammary gland NMLM... 36 4.8  
 W34557, W34557 mc58a05.rl Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 W98818, W98818 mf94e06.rl Soares mouse embryo NbME13.5 14.5 M... 36 4.8  
 AA008527, AA008527 mg85h01.rl Soares mouse embryo NbME13.5 14... 36 4.8  
 AA008734, AA008734 mg86h03.rl Soares mouse embryo NbME13.5 14... 36 4.8  
 AA510568, AA510568 vg33a10.rl Soares mouse mammary gland NbMM... 36 4.8  
 AA672524, AA672524 vo59e11.rl Soares mouse mammary gland NbMM... 36 4.8  
 AA052773, AA052773 mf24h01.rl Soares mouse embryo NbME13.5 14... 36 4.8  
 AA096626, AA096626 mo09h06.rl Life Tech mouse embryo 10 5dpc ... 36 4.8  
 AA124880, AA124880 mp73e06.rl Soares 2NbMT Mus musculus cDNA ... 36 4.8  
 AA198005, AA198005 mv12b09.rl GuayWoodford Beier mouse kidney... 36 4.8  
 AA624213, AA624213 vm98h06.rl Knowles Solter mouse blastocyst... 36 4.8  
 AA521863, AA521863 vi08b01.rl Barstead mouse myotubes MPLRB5 ... 36 4.8  
 AA692113, AA692113 vt19d03.rl Barstead mouse myotubes MPLRB5 ... 36 4.8  
 W71551, W71551 me39e11.rl Soares mouse embryo NbME13.5 14.5 M... 36 4.8

AA646501, AA646501 vn12g12.r1 Stratagene mouse heart (#937316... 36 4.8  
 AA607056, AA607056 vm95e05.r1 Knowles Solter mouse blastocyst... 36 4.8  
 AA163340, AA163340 ms65b10.r1 Stratagene mouse embryonic carc... 36 4.8  
 AA110893, AA110893 mm02b04.r1 Stratagene mouse kidney (#93731... 36 4.8

AI030290, AI030290 UI-R-C0-jb-d-01-0-UI.s1 UI-R-C0 Rattus nor... 293 1e-77  
 C71833, C71833 Rice cDNA, partial sequence (E0428\_1A) 44 0.017  
 AA926551, AA926551 TENS1173 T. cruzi epimastigote normalized ... 42 0.069  
 AA875699, AA875699 TENU0170 T. cruzi epimastigote normalized c... 42 0.069  
 AA567661, AA567661 HL01595.5prime HL Drosophila melanogaster ... 40 0.27  
 C74504, C74504 Rice cDNA, partial sequence (E31753\_1A) 40 0.27  
 AA698333, AA698333 HL04291.5prime HL Drosophila melanogaster ... 38 1.1  
 AA441429, AA441429 LD16359.5prime LD Drosophila melanogaster ... 38 1.1  
 N68770, N68770 TgESTzy35b12.r1 TgRH Tachyzoite cDNA Toxoplasma... 38 1.1  
 AA246440, AA246440 LD05311.5prime LD Drosophila melanogaster ... 38 1.1  
 AA801776, AA801776 GM12975.5prime GM Drosophila melanogaster ... 38 1.1  
 N69148, N69148 TgESTzy33d10.r1 TgRH Tachyzoite cDNA Toxoplasma... 38 1.1  
 AA536484, AA536484 LD17114.5prime LD Drosophila melanogaster ... 38 1.1  
 AA392544, AA392544 LD11451.5prime LD Drosophila melanogaster ... 38 1.1  
 AA202696, AA202696 LD03182.5prime LD Drosophila melanogaster ... 38 1.1  
 AA392367, AA392367 LD11287.5prime LD Drosophila melanogaster ... 38 1.1  
 AA264629, AA264629 LD08245.5prime LD Drosophila melanogaster ... 38 1.1  
 AA735318, AA735318 LD21104.5prime LD Drosophila melanogaster ... 38 1.1  
 AA264558, AA264558 LD08333.5prime LD Drosophila melanogaster ... 38 1.1  
 AA536476, AA536476 LD17106.5prime LD Drosophila Embryo Drosop... 38 1.1  
 AA957774, AA957774 UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor... 38 1.1  
 AA567991, AA567991 HL02092.5prime HL Drosophila melanogaster ... 38 1.1  
 AA957876, AA957876 UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor... 38 1.1  
 AA892488, AA892488 EST196291 Normalized rat kidney, Bento Soa... 38 1.1  
 AA699001, AA699001 HL06668.5prime HL Drosophila melanogaster ... 36 4.3  
 C19706, C19706 Rice cDNA, partial sequence (E10809\_1A) 36 4.3  
 D41773, RICS4574A Rice cDNA, partial sequence (S4574\_2A). 36 4.3  
 C40680, C40680 C.elegans cDNA clone yk247c4 : 5' end, single... 36 4.3  
 AA698625, AA698625 HL05354.5prime HL Drosophila melanogaster ... 36 4.3  
 C82819, C82819 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3  
 D46016, RICS10393A Rice cDNA, partial sequence (S10393\_3A). 36 4.3  
 AA536314, AA536314 LD16858.5prime LD Drosophila melanogaster ... 36 4.3  
 AA801012, AA801012 EST190509 Normalized rat muscle, Bento Soa... 36 4.3  
 D46541, RICS11289A Rice cDNA, partial sequence (S11289\_1A). 36 4.3  
 D47315, RICS12612A Rice cDNA, partial sequence (S12612\_1A). 36 4.3  
 AA735857, AA735857 GM09977.5prime GM Drosophila melanogaster ... 36 4.3  
 AA753921, AA753921 97BS0370 Rice Immature Seed Lambda ZAPII c... 36 4.3  
 D47243, RICS12505A Rice cDNA, partial sequence (S12505\_1A). 36 4.3  
 AA978395, AA978395 LD28411.5prime LD Drosophila melanogaster ... 36 4.3

D15134, RICC0136A Rice cDNA, partial sequence (C0136A). 36 4.3  
 D46483, RICS11185A Rice cDNA, partial sequence (S11185\_1A). 36 4.3  
 D46618, RICS11395A Rice cDNA, partial sequence (S11395\_1A). 36 4.3  
 D46659, RICS11457A Rice cDNA, partial sequence (S11457\_1A). 36 4.3  
 D46719, RICS11572A Rice cDNA, partial sequence (S11572\_1A). 36 4.3  
 D48579, RICS14880A Rice cDNA, partial sequence (S14880\_2A). 36 4.3  
 AA802334, AA802334 GM04219.5prime GM Drosophila melanogaster ... 36 4.3  
 D46066, RICS10470A Rice cDNA, partial sequence (S10470\_1A). 36 4.3  
 D47037, RICS12104A Rice cDNA, partial sequence (S12104\_1A). 36 4.3  
 D46874, RICS11807A Rice cDNA, partial sequence (S11807\_2A). 36 4.3  
 D47174, RICS12340A Rice cDNA, partial sequence (S12340\_2A). 36 4.3  
 T04578, T04578 625 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 36 4.3  
 C83675, C83675 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3  
 D47950, RICS13762A Rice cDNA, partial sequence (S13762\_1A). 36 4.3  
 R90044, R90044 16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 4.3  
 D46994, RICS12013A Rice cDNA, partial sequence (S12013\_2A). 36 4.3  
 AA440820, AA440820 LD15713.5prime LD Drosophila melanogaster ... 36 4.3  
 C72089, C72089 Rice cDNA, partial sequence (E0963\_1A) 36 4.3  
 Z84004, SSZ84004 S.scrofa mRNA; expressed sequence tag (5'; ... 36 4.3  
 D47519, RICS13070A Rice cDNA, partial sequence (S13070\_1A). 36 4.3  
 C19735, C19735 Rice cDNA, partial sequence (E10858\_1A) 36 4.3  
 D47231, RICS12462A Rice cDNA, partial sequence (S12462\_1A). 36 4.3  
 D47147, RICS12293A Rice cDNA, partial sequence (S12293\_1A). 36 4.3  
 AA950198, AA950198 LD30147.5prime LD Drosophila melanogaster ... 36 4.3  
 Z47624, ATTS4480 A. thaliana transcribed sequence; clone TAI... 36 4.3  
 D45955, RICS10259A Rice cDNA, partial sequence (S10259\_1A). 36 4.3  
 D47137, RICS12280A Rice cDNA, partial sequence (S12280\_1A). 36 4.3  
 D69927, CELK093H2F C.elegans cDNA clone yk93h2 : 5' end, sin... 36 4.3  
 AA392275, AA392275 LD11117.5prime LD Drosophila melanogaster ... 36 4.3

## SEQ ID NO:546

D87455, D87455 Human mRNA for KIAA0266 gene, complete cds 1164 0.0  
 Z99129, HS425C14 Human DNA sequence from clone 425C14 on chr... 42 0.20  
 D90900, D90900 Synechocystis sp. PCC6803 complete genome, 2/... 40 0.80  
 Z74281, SCYDL233W S.cerevisiae chromosome IV reading frame O... 38 3.1  
 AL021528, HS394P21 Homo sapiens DNA sequence from PAC 394P21... 38 3.1  
 Z49155, HSL83D3 Human DNA from cosmid L83d3, Huntington's Di... 38 3.1  
 U33761, HSU33761 Human cyclin A/CDK2-associated p45 (Skp2) mR... 38 3.1  
 AF052832, AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 38 3.1  
 Z98600, SPAC20G4 S.pombe chromosome I cosmid c20G4 38 3.1

Y09438, SPHUSPLUS *S.pombe* *hus1+* gene 38 3.1  
D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

## HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0  
AA824593, AA824593 oc83d10.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 670 0.0  
AA954862, AA954862 op20c03.s1 NCI\_CGAP\_Co12 Homo sapiens cDNA... 581 e-164  
T16360, T16360 NIB1193 Normalized infant brain, Bento Soares ... 517 e-145  
R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143  
AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142  
AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104  
R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103  
AA249614, AA249614 k3041.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65  
AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44  
AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5  
AA992442, AA992442 or85h03.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79  
AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035  
W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035  
AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035  
AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2  
AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2  
AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2  
AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2  
AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2  
AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2  
AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2  
AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9  
C40718, C40718 *C.elegans* cDNA clone yk247f9 : 5' end, single... 36 1.9  
AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9  
AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 *Mus musculus* fibroblast growth factor homolo... 42 0.35  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35  
 AF020738, AF020738 *Mus musculus* fibroblast growth factor-rela... 42 0.35  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4  
 Z46966, MMIMOGN44 *M. musculus* mRNA for imogen 44. 40 1.4  
 AC004301, AC004301 *Drosophila melanogaster* DNA sequence (P1 D... 40 1.4  
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 40 1.4

#### HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0  
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143  
 AA551799, AA551799 nk04a11.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 363 4e-98  
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17  
 AA888147, AA888147 04h11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.67  
 AA946650, AA946650 oq38h09.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.67  
 AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA806381, AA806381 oc22g05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.67  
 AA577174, AA577174 nm86e11.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 40 0.67  
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.67  
 AA262229, AA262229 zs25b12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.67  
 AA969632, AA969632 op38h05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.67  
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.67  
 AI005324, AI005324 ou13h07.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.67  
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.67  
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA814296, AA814296 nz07d08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.67  
 AA873216, AA873216 oh70f04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.67  
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67  
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.67  
 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.67  
 AA974988, AA974988 on59b06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.67  
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67  
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67  
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.67  
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.67  
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.67  
 AA877455, AA877455 ob33g01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.67  
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.67

AA903406, AA903406 ok62c11.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.67  
 AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67  
 AA927863, AA927863 om18a08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.67  
 AA587486, AA587486 nn84e09.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA .... 40 0.67  
 W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.67  
 AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.67  
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67  
 AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA872272, AA872272 oh72a11.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.67  
 W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.67  
 N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.67  
 N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.67  
 AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA826741, AA826741 85f12.s1 NCI\_CGAP\_Pr24 Homo sapiens cDNA... 40 0.67  
 AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.67  
 AI040354, AI040354 oy33d12.x1 Soares\_parathyroid\_tumor\_NbHPA ... 40 0.67  
 AA573297, AA573297 nk98d09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.67  
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.67  
 AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67  
 AI005204, AI005204 ou60c12.x1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.67  
 N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.67  
 AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA804907, AA804907 oa89a01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.67  
 AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.67  
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67  
 AA618498, AA618498 np30a11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 40 0.67  
 AA503727, AA503727 ne49g02.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.67  
 AA514777, AA514777 ni24b01.s1 NCI\_CGAP\_Co4 Homo sapiens cDNA ... 40 0.67  
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.67  
 AA770473, AA770473 ah89h06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.67  
 AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.67  
 AA262162, AA262162 zs25b12.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.67  
 AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 2.6  
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.6  
 AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 2.6  
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.6  
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.6  
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.6  
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6  
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6  
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43  
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.24  
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24  
AA103139, AA103139 mol17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24  
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.24  
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24  
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24  
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.24  
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24  
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.24  
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24  
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24  
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24  
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.24  
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24  
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.24  
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.24  
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24  
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24  
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24  
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.24  
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.24  
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24  
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.24  
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24  
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24  
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24  
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.24  
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.94  
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7  
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7  
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7  
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7  
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7  
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7  
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7  
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7  
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7  
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7



AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.7  
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.7  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.7  
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7  
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.7  
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.7  
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7  
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.7  
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.7  
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.7  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.7  
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7  
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.7  
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7  
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.7

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.053  
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84  
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.84  
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84  
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84  
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.84  
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.84  
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.84  
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.84  
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.84  
 AA660819, AA660819 00713 MtrHE Medicago truncatula cDNA 5' ... 38 0.84  
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84  
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.84  
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84  
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.84  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.3  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.3  
 D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.3  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.3  
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.3  
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.3  
 D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.3  
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.3  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.3  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.3  
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.3  
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.3  
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.3

SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34  
 U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.34  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3  
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

## HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0  
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143  
 AA551799, AA551799 nk04a11.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 363 3e-98  
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.16  
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.64  
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64  
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.64  
 AA573297, AA573297 nk98d09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.64  
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.64  
 AA888147, AA888147 04h11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.64  
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.64  
 AA877455, AA877455 ob33g01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.64  
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.64  
 AA514777, AA514777 ni24b01.s1 NCI\_CGAP\_Co4 Homo sapiens cDNA ... 40 0.64  
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.5  
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.5  
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.5  
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.5  
 AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 2.5  
 AA852281, AA852281 NHTBCael1g05r1 Normal Human Trabecular Bon... 38 2.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43  
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.23  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.23  
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.23  
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.23  
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.23  
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.23  
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.23  
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.91  
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6  
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6  
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.6  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.6  
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.6  
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.6  
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6  
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.6  
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6  
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.6  
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6  
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.6  
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.6  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.6  
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.6  
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.6  
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.6  
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.6  
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.6  
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.6  
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6  
 AA089210, AA089210 mio05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.6  
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.6  
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.6

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.052  
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.81  
 AA660819, AA660819 00713 MtrHE Medicago truncatula cDNA 5' ... 38 0.81  
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.81  
 D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.2  
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.2  
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.2  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2  
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.2

D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.2  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.2  
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.2  
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.2  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.2  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.2  
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.2

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U79271, HSU79271 Human clones 23920 and 23921 mRNA sequence 650 0.0  
 AC000395, AC000395 Genomic sequence from Human 9q34, complete... 42 0.28  
 AC004636, AC004636 Homo sapiens chromosome 5, P1 clone 1268h6... 42 0.28  
 M94579, HUMCEL Human carboxyl ester lipase (CEL) gene, comple... 42 0.28  
 AC002097, AC002097 Homo sapiens chromosome 9q34, clone 246H5,... 42 0.28  
 AB006709, AB006709 Vibrio alginolyticus rpoN gene for RNA po... 42 0.28  
 Z47074, CEK07C10 Caenorhabditis elegans cosmid K07C10, compl... 40 1.1  
 AC004755, AC004755 Homo sapiens chromosome 19, fosmid 37502, ... 40 1.1  
 Z28051, SCYKL051W S.cerevisiae chromosome XI reading frame O... 40 1.1  
 AF022655, AF022655 Homo sapiens cep250 centrosome associated ... 40 1.1  
 AB006708, AB006708 Arabidopsis thaliana genomic DNA, chromos... 40 1.1  
 AF049105, AF049105 Homo sapiens centrosomal Nek2-associated p... 40 1.1  
 Z28050, SCYKL050C S.cerevisiae chromosome XI reading frame O... 40 1.1  
 X75781, SCXI286K S.cerevisiae chromosome XI (28.6 kb) DNA fo... 40 1.1  
 Y16899, DMY16899 Drosophila melanogaster mRNA for optomotor-... 38 4.3  
 M87854, RATBARK1 Rattus norvegicus beta-adrenergic receptor k... 38 4.3  
 M74822, RATMHTLL Rat MHC class I TL-like protein gene, comple... 38 4.3  
 M80776, HUMBARK1A Human beta-adrenergic receptor kinase 1 mRN... 38 4.3  
 D84549, YSACA Candida tropicalis DNA for carnitine acetyltra... 38 4.3  
 L23127, RATRMCI Rattus norvegicus germline MHC class I gene, ... 38 4.3  
 AC004257, AC004257 Homo sapiens chromosome 19, cosmid R33209,... 38 4.3  
 U70850, CELF28F9 Caenorhabditis elegans cosmid F28F9 38 4.3  
 U88309, CELT23B3 Caenorhabditis elegans cosmid T23B3 38 4.3  
 X53421, DVCHOS18 D. virilis s18, s15, s19, s16 chorion prote... 38 4.3  
 D89245, D89245 Schizosaccharomyces pombe mRNA, partial cds, ... 38 4.3  
 AF009623, AF009623 Parascaris univalens PUMA1 (puma1) mRNA, c... 38 4.3  
 S48813, S48813 beta-adrenergic receptor kinase [rats, brain, ... 38 4.3  
 Z67883, CEK02A4 Caenorhabditis elegans cosmid K02A4, complet... 38 4.3  
 U90567, GGU90567 Gallus gallus glutamine rich protein mRNA, p... 38 4.3  
 M98498, BOVEZRINA Bos taurus ezrin mRNA, complete cds. 38 4.3  
 M34073, MUSMHT10C Mus musculus (clone T10-c) MHC class I cell... 38 4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3  
 X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3  
 U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3  
 U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2... 38 4.3

## HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0  
 AA886109, AA886109 ny44f05.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA... 656 0.0  
 AA829894, AA829894 oe51e12.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 650 0.0  
 AA879456, AA879456 oj91g03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 650 0.0  
 AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0  
 AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0  
 AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0  
 W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0  
 N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0  
 AI033069, AI033069 ow93f02.s1 Soares\_fetal\_liver\_spleen\_1NFLS... 642 0.0  
 AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0  
 N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180  
 N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180  
 H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180  
 AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180  
 R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178  
 AA744290, AA744290 ny51d02.s1 NCI\_CGAP\_Pr18 Homo sapiens cDNA... 626 e-177  
 AI038590, AI038590 ox34e03.s1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 624 e-177  
 AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177  
 AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176  
 AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173  
 R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167  
 R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167  
 H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165  
 R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164  
 AA910762, AA910762 ol25h06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 559 e-157  
 AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156  
 AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153  
 R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151  
 H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150  
 N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149  
 D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129  
 H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122  
 AA971254, AA971254 op73c08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 442 e-122  
 W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118  
 AA878973, AA878973 oj26d11.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 389 e-106  
 AA715235, AA715235 nv10g01.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96  
 AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74  
 AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69  
 AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41  
 T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'. 170 2e-40  
 N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'. 165 1e-38  
 AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18  
 AI038890, AI038890 ox84g12.x1 Soares\_senescent\_fibroblasts\_Nb... 40 0.53  
 D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08. 38 2.1  
 AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1  
 AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen 1NFLS... 38 2.1  
 AA742364, AA742364 ny89c12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.1  
 AA907234, AA907234 ol03h08.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 2.1  
 T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1  
 AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1  
 AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1  
 AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1  
 AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1  
 W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1  
 AI039908, AI039908 ox25f07.x1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 38 2.1  
 AA280664, AA280664 zs99f09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.1  
 AA973566, AA973566 oo46f09.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 2.1  
 N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'. 38 2.1  
 AA995707, AA995707 os29c09.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 38 2.1  
 AI016407, AI016407 ot72e09.s1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 38 2.1  
 N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'. 38 2.1  
 AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1  
 AA938631, AA938631 oo96f07.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 38 2.1  
 AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103  
 AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44  
 AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41  
 AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38  
 AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10  
 AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07  
 AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19  
 AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19  
 AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75  
 AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75  
 W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75  
 AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AI019772, AI019772 ua90h02.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA472253, AA472253 vh10g05.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA230895, AA230895 mw14g07.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.0  
 W18052, W18052 mb83g03.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.0  
 AA797681, AA797681 vx66c12.r1 Stratagene mouse skin (#937313)... 36 3.0  
 W66734, W66734 me26g05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0  
 AA968020, AA968020 uh07g01.r1 Soares mouse hypothalamus NMHy ... 36 3.0  
 AA051644, AA051644 mj55d12.r1 Soares mouse embryo NbME13.5 14... 36 3.0  
 AA162797, AA162797 mr29g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA549644, AA549644 vk80f08.s1 Knowles Solter mouse 2 cell Mus... 36 3.0  
 AA273295, AA273295 vc01e01.r1 Soares mouse lymph node NbMLN M... 36 3.0  
 AA048480, AA048480 mj33d08.r1 Soares mouse embryo NbME13.5 14... 36 3.0  
 AA098207, AA098207 mn83d01.r1 Stratagene mouse Tcell 937311 M... 36 3.0  
 AA027381, AA027381 mi05c06.r1 Soares mouse placenta 4NbMP13.5... 36 3.0  
 AA544474, AA544474 vk33h06.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA416466, AA416466 vd15c09.s1 Knowles Solter mouse 2 cell Mus... 36 3.0  
 AA285999, AA285999 vb88h08.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA175025, AA175025 ms85f06.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA544386, AA544386 vk33f06.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA175557, AA175557 ms96g04.r1 Soares mouse 3NbMS Mus musculus... 36 3.0  
 AA711924, AA711924 vu59f09.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA734052, AA734052 vv22c10.r1 Stratagene mouse heart (#937316... 36 3.0  
 W53738, W53738 md12a12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0  
 AA611837, AA611837 vo82a06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.0  
 AA879531, AA879531 vv96f06.r1 Soares mouse mammary gland NbMM... 36 3.0  
 AA288625, AA288625 vb23g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0

AA784124, AA784124 d2b06a1.fl Aspergillus nidulans 24hr asexu... 38 0.67  
 AI044911, AI044911 UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor... 36 2.6  
 AA550452, AA550452 1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 2.6  
 F20017, ATTS6056 A. thaliana transcribed sequence; clone TAP... 36 2.6  
 AA786697, AA786697 k5d01a1.fl Aspergillus nidulans 24hr asexu... 36 2.6  
 AA433457, AA433457 SW3ICA2345SK Brugia malayi infective larva... 36 2.6

SEQ ID NO:550

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.20  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.20  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.20  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 0.80

AC004301, AC004301 *Drosophila melanogaster* DNA sequence (P1 D... 40 0.80  
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 40 0.80  
 Y14330, HSY14330 *Homo sapiens* partial mRNA for jagged2 protein 38 3.2  
 AF003521, AF003521 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2  
 AF029778, AF029778 *Homo sapiens* Jagged2 (JAG2) mRNA, complete... 38 3.2  
 AF020201, AF020201 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2  
 Z71523, SCYNL247W *S.cerevisiae* chromosome XIV reading frame ... 38 3.2  
 AF029779, AF029779 *Homo sapiens* hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2  
 U70049, RNU70049 *Rattus norvegicus* jagged2 precursor gene, pa... 38 3.2  
 X96722, SCCHXIVL *S.cerevisiae* DNA region from chromosome XIV... 38 3.2  
 AF005938, AF005938 *Cavia porcellus* L-type voltage-dependent c... 38 3.2  
 X78972, SBSTRBF *S.blauensis* ISP 5564 genes strB and strF 38 3.2  
 X94912, HSPR22 *H.sapiens* Pr22 gene 38 3.2

#### HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT *Homo sapiens* ... 650 0.0  
 AA348243, AA348243 EST54707 Hippocampus I *Homo sapiens* cDNA 5... 513 e-144  
 AA551799, AA551799 nk04a11.s1 NCI\_CGAP\_Co2 *Homo sapiens* cDNA ... 363 2e-98  
 AA327309, AA327309 EST30621 Colon I *Homo sapiens* cDNA 5' end 353 2e-95  
 AA344913, AA344913 EST50856 Gall bladder II *Homo sapiens* cDNA... 337 1e-90  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) *Homo*... 317 1e-84  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) *Homo*... 317 1e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR *Homo sapie*... 42 0.098  
 AI005204, AI005204 ou60c12.x1 NCI\_CGAP\_Br2 *Homo sapiens* cDNA ... 40 0.39  
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39  
 AI005324, AI005324 ou13h07.x1 Soares\_NFL\_T\_GBC\_S1 *Homo sapien*... 40 0.39  
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 *Homo sapiens* c... 40 0.39  
 AA262162, AA262162 zs25b12.r1 NCI\_CGAP\_GCB1 *Homo sapiens* cDNA... 40 0.39  
 AA824270, AA824270 aj29f01.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA826741, AA826741 85f12.s1 NCI\_CGAP\_Pr24 *Homo sapiens* cDNA... 40 0.39  
 AA813115, AA813115 aj44d06.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39  
 AA804907, AA804907 oa89a01.s1 NCI\_CGAP\_GCB1 *Homo sapiens* cDNA... 40 0.39  
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA618498, AA618498 np30a11.s1 NCI\_CGAP\_Pr22 *Homo sapiens* cDNA... 40 0.39  
 AA503727, AA503727 ne49g02.s1 NCI\_CGAP\_Co3 *Homo sapiens* cDNA ... 40 0.39  
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39  
 AA759377, AA759377 ah54a10.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA629243, AA629243 zu77e03.s1 Soares testis NHT *Homo sapiens* ... 40 0.39  
 AA903406, AA903406 ok62c11.s1 NCI\_CGAP\_GC4 *Homo sapiens* cDNA ... 40 0.39  
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39



AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.39  
AA577174, AA577174 nm86e11.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 40 0.39  
AA969632, AA969632 op38h05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.39  
N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.39  
AA974988, AA974988 on59b06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.39  
W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.39  
N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.39  
AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.39  
AA814296, AA814296 nz07d08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.39  
AA806381, AA806381 oc22g05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.39  
AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.39  
W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.39  
AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.39  
AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.39  
AA927863, AA927863 om18a08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.39  
AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.39  
W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.39  
AA262229, AA262229 zs25b12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.39  
AA587486, AA587486 nn84e09.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.39  
AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39  
AA872272, AA872272 oh72a11.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.39  
W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.39  
N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.39  
N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.39  
AI040354, AI040354 oy33d12.x1 Soares\_parathyroid\_tumor\_NbHPA ... 40 0.39  
AA946650, AA946650 oq38h09.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.39  
AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.39  
AA873216, AA873216 oh70f04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.39  
R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 1.5  
H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 1.5  
AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 1.5  
AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 1.5  
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 1.5  
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 1.5  
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 6e-44  
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.14  
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.14  
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.14

AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.14  
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.14  
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.14  
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.14  
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.14  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.14  
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.14  
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.14  
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.14  
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.14  
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14  
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.14  
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.14  
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.14  
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.14  
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14  
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.14  
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.14  
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.55  
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2  
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 2.2  
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 2.2  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 2.2  
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 2.2  
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 2.2  
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2  
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2  
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 2.2  
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 2.2  
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.2  
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 2.2  
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 2.2  
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 2.2  
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 2.2  
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 2.2  
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 2.2

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AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031  
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.48  
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48  
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48  
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48  
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48  
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48  
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48  
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48  
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48  
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48  
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 1.9  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9  
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9  
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 1.9  
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9  
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4  
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

## HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

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 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17  
 AA877455, AA877455 ob33g01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.68  
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.68  
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 AA573297, AA573297 nk98d09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.68  
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.68  
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 AA888147, AA888147 04h11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.68  
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.68  
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 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.7  
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 AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 2.7  
 R14449, R14449 yf81h09.r1 Homo sapiens cDNA clone 29034 5'. 38 2.7  
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.7

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 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24  
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24  
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 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.97  
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 0.97  
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 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.8  
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 3.8  
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.8  
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 3.8  
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 3.8

AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.8  
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 3.8  
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AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 3.8  
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.8  
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.8  
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8  
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8  
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8  
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 3.8  
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.8  
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.8  
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.8  
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 3.8  
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 3.8  
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8  
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.8  
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.8  
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.8  
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 3.8  
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 3.8  
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 3.8  
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 3.8  
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 3.8  
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.8  
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 3.8  
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8  
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.8  
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 3.8  
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8  
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.8  
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.8  
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.8  
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 3.8  
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 3.8  
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 3.8  
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 3.8  
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.8  
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 3.8  
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8  
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.8

276X

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055  
 AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22  
 Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22  
 AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22  
 AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22  
 H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22  
 AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22  
 Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22  
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86  
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86  
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86  
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.4  
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4  
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.4  
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4  
 AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4  
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4  
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4  
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4  
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4  
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4  
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4  
 D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.4  
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4  
 AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.4  
 D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.4

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U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38  
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38  
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38  
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5  
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5  
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

## HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0  
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

276Y

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 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95  
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90  
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84  
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.18  
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72  
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72  
 AA877455, AA877455 ob33g01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.72  
 AA573297, AA573297 nk98d09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.72  
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 AA888147, AA888147 04h11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.72  
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 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8  
 N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8  
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.8  
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8  
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8  
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8  
 AA948291, AA948291 oq34d02.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 38 2.8

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43  
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.26  
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26  
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.26  
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26  
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.26  
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 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 1.0  
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 1.0  
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 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 4.0  
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 4.0  
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 4.0  
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 4.0  
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 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0  
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 4.0  
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 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 4.0  
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 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 4.0  
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.0  
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 4.0  
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0  
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 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 4.0  
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 AA103139, AA103139 mol17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 4.0  
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 4.0  
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 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 4.0  
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 4.0  
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 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 4.0  
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 4.0  
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 4.0



AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.058  
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.90  
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.90  
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.90  
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.6  
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.6  
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.6  
AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.6  
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.6  
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6  
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.6  
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.6  
D45997, RICS10346A Rice cDNA, partial sequence (S10346\_1A). 36 3.6  
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6  
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6  
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.6  
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6  
D46069, RICS10475A Rice cDNA, partial sequence (S10475\_1A). 36 3.6  
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.6

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Z99297, HS262D12 Homo sapiens DNA sequence from PAC 262D12 o... 1963 0.0  
Z81540, CEF46B3 Caenorhabditis elegans cosmid F46B3, complet... 40 0.89  
U67488, U67488 Methanococcus jannaschii section 30 of 150 of ... 38 3.5  
AE000786, AE000786 Borrelia burgdorferi plasmid lp28-2, compl... 38 3.5  
L02053, OMMGSHTR1 Ommastrephes sloani glutathione transferase... 38 3.5  
AC004521, ATAC004521 Arabidopsis thaliana chromosome II BAC F... 38 3.5  
L41250, DROGPDHN Drosophila nebulosa glycerol-3-phosphate deh... 38 3.5  
AE000619, HPAE000619 Helicobacter pylori section 97 of 134 of... 38 3.5  
U39720, Mycoplasma genitalium ackA, licA, mucB, rpL10, rpL32... 38 3.5  
AC004533, HUAC004533 Homo sapiens Chromosome 16 BAC clone CIT... 38 3.5  
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

## HUMAN ESTs

W02630, W02630 za52c02.r1 Soares fetal liver spleen 1NFLS Hom... 1009 0.0  
AA557183, AA557183 n174f12.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 874 0.0  
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AA976975, AA976975 oq26g11.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 854 0.0  
AA449515, AA449515 zx06b11.r1 Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0  
 AA909198, AA909198 ol12d06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 831 0.0  
 W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0  
 W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0  
 W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0  
 AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0  
 H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0  
 W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0  
 AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0  
 AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0  
 AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0  
 AA662309, AA662309 nu97c11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 668 0.0  
 W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0  
 N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176  
 N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165  
 AA251287, AA251287 zs04c06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 583 e-164  
 AA971082, AA971082 op70h01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 567 e-160  
 W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159  
 AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157  
 AA729063, AA729063 nw22f08.s1 NCI\_CGAP\_GCB0 Homo sapiens cDNA... 557 e-157  
 AA987313, AA987313 or81h06.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 553 e-155  
 AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152  
 AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148  
 N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146  
 AA947355, AA947355 od86e12.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA ... 504 e-140  
 AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127  
 AA742964, AA742964 ny15d01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 454 e-126  
 AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125  
 W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123  
 W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121  
 AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109  
 N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106  
 N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104  
 AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99  
 AA936553, AA936553 on23g11.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 361 9e-98  
 N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95  
 AA834628, AA834628 od98a10.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA ... 341 8e-92  
 AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92  
 AA909616, AA909616 ol09d06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 341 8e-92  
 H69662, H69662 yr92b03.s1 Homo sapiens cDNA clone 212717 3'. 321 8e-86  
 AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84  
 AA911960, AA911960 oh88g08.s1 NCI\_CGAP\_Co8 Homo sapiens cDNA ... 317 1e-84  
 AA969099, AA969099 op55e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 303 2e-80  
 AA766191, AA766191 oa12g08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 212 5e-53  
 AA689312, AA689312 nx05e10.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586 zv93e05.r1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44  
 AA418570, AA418570 zv93e05.s1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44  
 AA534939, AA534939 nf82f03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 167 3e-39  
 AA888430, AA888430 nw74e05.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA... 167 3e-39  
 N50003, N50003 yv24d04.r1 Homo sapiens cDNA clone 243655 5' s... 149 6e-34  
 AA535102, AA535102 nf84f06.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 135 1e-29  
 AA262335, AA262335 zr71g03.s1 Soares NhHMPu S1 Homo sapiens c... 129 6e-28  
 AA766681, AA766681 oa34c05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 105 9e-21  
 AA761492, AA761492 nz27a05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 101 1e-19  
 AA688350, AA688350 nv15a05.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 90 5e-16  
 AA347041, AA347041 EST53285 Fetal heart II Homo sapiens cDNA ... 76 8e-12  
 T94395, T94395 ye35e02.s1 Homo sapiens cDNA clone 119738 3'. 46 0.007  
 AA833565, AA833565 aj46a02.s1 Soares testis NHT Homo sapiens ... 46 0.007  
 AA095460, AA095460 l4630.seq.F Fetal heart, Lambda ZAP Expres... 40 0.43  
 AA904415, AA904415 ok07e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 40 0.43  
 AI018800, AI018800 ov32h04.x1 Soares\_testis\_NHT Homo sapiens ... 38 1.7  
 AA631083, AA631083 nq77e07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 1.7

AA399772, AA399772 vd70g05.r1 Beddington mouse embryonic regi... 347 5e-94  
 AA467106, AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 309 1e-82  
 AI046844, AI046844 uh55c11.r1 Soares mouse embryonic stem cel... 208 3e-52  
 AA475075, AA475075 vh11g05.r1 Soares mouse mammary gland NbMM... 194 4e-48  
 AA646094, AA646094 vs31e06.r1 Stratagene mouse Tcell 937311 M... 186 1e-45  
 AA390020, AA390020 vb30e07.r1 Soares mouse lymph node NbMLN M... 170 6e-41  
 AA245553, AA245553 my52g04.r1 Barstead mouse pooled organs MP... 170 6e-41  
 AA930741, AA930741 vs57b02.r1 Stratagene mouse skin (#937313)... 155 4e-36  
 W62610, W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 117 8e-25  
 AA239270, AA239270 my40e01.r1 Barstead mouse pooled organs MP... 109 2e-22  
 AA015148, AA015148 mh16e01.r1 Soares mouse placenta 4NbMP13.5... 54 1e-05  
 AA764095, AA764095 vw09h02.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.61  
 AA238570, AA238570 my35h02.r1 Barstead mouse pooled organs MP... 38 0.61  
 AA600576, AA600576 vm75f08.r1 Knowles Solter mouse blastocyst... 38 0.61  
 AA636273, AA636273 vq76a10.s1 Knowles Solter mouse 2 cell Mus... 36 2.4  
 AA051407, AA051407 mj41f08.r1 Soares mouse embryo NbME13.5 14... 36 2.4  
 AA823136, AA823136 vw41b03.r1 Soares mouse mammary gland NbMM... 36 2.4  
 W83831, W83831 mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4  
 D77944, MUSC0D06 Mouse embryonal carcinoma F9 cell cDNA, C0D06 36 2.4  
 AA915408, AA915408 vz29h04.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.4  
 AI047229, AI047229 uh63a09.r1 Soares mouse embryonic stem cel... 36 2.4  
 AA271880, AA271880 va73d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4  
 AA475165, AA475165 vg95f01.r1 Barstead mouse pooled organs MP... 36 2.4  
 AA619774, AA619774 vl58a05.s1 Knowles Solter mouse 2 cell Mus... 36 2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4  
 AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4  
 W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4  
 AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4  
 AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4  
 AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4  
 AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus musc... 36 2.4  
 AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4  
 AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14  
 F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54  
 H91505, H91505 SWMFCA089SK Brugia malayi microfilaria cDNA (S... 36 2.1  
 AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1  
 AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1  
 AI008397, AI008397 EST202848 Normalized rat embryo, Bento Soa... 36 2.1

## SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0  
 Z46940, HSPRMTNP2 H.sapiens PRM1 gene, PRM2 gene and TNP2 gene 44 0.048  
 U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19  
 U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19  
 AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19  
 AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19  
 AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19  
 U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19  
 Z97343, ATFC8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75  
 L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75  
 M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75  
 L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75  
 J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75  
 M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75  
 X72711, MMREPCFC M.musculus mRNA for replication factor C, l... 38 3.0  
 M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0  
 U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0  
 AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0  
 J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0  
 J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0  
 X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0  
 X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0  
 D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0  
 Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0  
 D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-)-met... 38 3.0  
 Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0  
 L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0  
 U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0  
 U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0  
 K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0  
 Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0  
 U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0  
 Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

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AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0  
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005  
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019  
 AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073  
 X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.29  
 U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29  
 X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29  
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29  
 Z74201, SCYDL153C S.cerevisiae chromosome IV reading frame O... 42 0.29  
 U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29  
 Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29  
 X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29  
 X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29  
 L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29  
 U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 1.1  
 S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1  
 U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1  
 Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1  
 U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 1.1

- AF050157, MMHC135G15 *Mus musculus* major histocompatibility lo... 40 1.1
- X58857, SCPH22 *S.cerevisiae* PPH22 gene for protein phosphat... 40 1.1
- X79379, SCPROIS *S.cerevisiae* gene for proline isomerase 40 1.1
- Z68341, CEF01G4 *Caenorhabditis elegans* cosmid F01G4, complet... 40 1.1
- M17192, MUSHOX1 Mouse homeodomain protein (Hox1.1) mRNA, comp... 40 1.1
- U50307, CELF43H9 *Caenorhabditis elegans* cosmid F43H9. 40 1.1
- S73144, S73144 bone sialoprotein [cattle, fetal bone cells, m... 40 1.1
- L34569, YSCFPR3A *Saccharomyces cerevisiae* (clone pBYNG1) prol... 40 1.1
- D78303, D78303 *Rattus norvegicus* YT521 mRNA for RNA splicing... 40 1.1
- X83276, SCDNAIV *S.cerevisiae* DNA for ORFs from chromosome IV 40 1.1
- U54558, HSU54558 Human translation initiation factor eIF3 p66... 40 1.1
- Z50109, CEC09H10 *Caenorhabditis elegans* cosmid C09H10, compl... 40 1.1
- X56983, EAVATP1 *E.arvense* gene for catalytic 70kDa V-ATPase ... 40 1.1
- AB011125, AB011125 *Homo sapiens* mRNA for KIAA0553 protein, p... 40 1.1
- Z46373, SC8248 *S.cerevisiae* chromosome XIII cosmid 8248 40 1.1
- AF039042, CELZK697 *Caenorhabditis elegans* cosmid ZK697 40 1.1
- Z28028, SCYKL028W *S.cerevisiae* chromosome XI reading frame O... 40 1.1
- AC005266, AC005266 *Homo sapiens* chromosome 19, cosmid F23465,... 38 4.5
- U60822, HSU60822 Human dystrophin (DMD) gene, exons 7, 8 and ... 38 4.5
- AJ003141, HVAJ3141 *Hordeum vulgare* mRNA for stress-related p... 38 4.5
- M26250, CRAGAP43 Goldfish (*C.auratus*) growth-associated prote... 38 4.5
- X95267, GGRYR3 *G.gallus* mRNA for ryanodine receptor type 3 38 4.5
- L37092, MUSCDPK *Mus musculus* cyclin-dependent kinase homology... 38 4.5
- Z72507, CEF17C11 *Caenorhabditis elegans* cosmid F17C11, compl... 38 4.5
- U29608, DMU29608 *Drosophila melanogaster* large tumor suppress... 38 4.5
- Z49072, CET24A11 *Caenorhabditis elegans* cosmid T24A11, compl... 38 4.5
- M83142, RATBGASTR *Rattus norvegicus* beta-galactoside-alpha 2,... 38 4.5
- Z20656, HSCAMHCA *Homo sapiens* of cardiac alpha-myosin heavy ... 38 4.5
- M82937, YSACS2A *Candida albicans* chitin synthase 2 (CHS2) gen... 38 4.5
- U28888, MMU28888 *Mus musculus* neurogenic differentiation fact... 38 4.5
- S66408, S66408 c-erbB=proto-oncogene {exon 1, promoter} [chic... 38 4.5
- AC002396, AC002396 *Arabidopsis thaliana* chromosome I BAC F3I6... 38 4.5
- AE000665, MMAE000665 *Mus musculus* TCR beta locus from bases 5... 38 4.5
- L39837, DROWARTS *Drosophila melanogaster* tumor supressor (war... 38 4.5
- AG000377, AG000377 *Homo sapiens* genomic DNA, 21q region, clo... 38 4.5
- X05632, HSMHCAG1 Human alpha-MHC gene for myosin heavy chain... 38 4.5
- AC002108, AC002108 Genomic sequence from Mouse 4, complete se... 38 4.5
- U37219, HSU37219 Human cyclophilin-like protein CyP-60 mRNA, ... 38 4.5
- M58633, MUP58GTA Mouse p58/GTA protein kinase mRNA, complete... 38 4.5
- M25162, HUMMYHC08 Human cardiac alpha-myosin heavy chain (MYH... 38 4.5
- Z46259, SCRPD3COS *S.cerevisiae* FY1676 RPD3 gene. 38 4.5
- U09558, LJU09558 *Lactobacillus johnsonii* ATCC 11506 insertion... 38 4.5
- U66160, MMUSC104 *Mus musculus* extracellular matrix associated... 38 4.5
- Z73126, SCYLL021W *S.cerevisiae* chromosome XII reading frame ... 38 4.5
- U83981, HSU83981 *Homo sapiens* apoptosis associated protein (G... 38 4.5

U59897, MRU59897 *Macropus robustus* hypoxanthine phosphoribosy... 38 4.5  
 D38256, YSCSCT1 Yeast gene for suppressor of ctr mutation 38 4.5  
 X69838, HSG9A *H.sapiens* mRNA for G9a 38 4.5  
 X52952, RNCMOSO Rat mRNA for c-mos 38 4.5  
 U37221, HSU37221 Human cyclophilin-like protein mRNA, partial... 38 4.5  
 X65880, DPRH4OP1 *D.pseudoobscura* rh4 opsin gene, exon 1 38 4.5  
 U58971, NTU58971 *Nicotiana tabacum* calmodulin-binding protein... 38 4.5  
 Z35773, SCYBL012C *S.cerevisiae* chromosome II reading frame O... 38 4.5  
 X67668, MMHMG2 *M.musculus* mRNA for high mobility group 2 pro... 38 4.5  
 L81727, HSL81727 *Homo sapiens* (subclone 1\_d5 from P1 H69) DNA... 38 4.5  
 AL023800, HS833B2 Human DNA sequence \*\*\* SEQUENCING IN PROGR... 38 4.5  
 X62438, HVPERO *H.vulgare* mRNA for peroxidase 38 4.5  
 AC004096, AC004096 Mouse Cosmid ma66a100 from 14D1-D2, comple... 38 4.5  
 AL008980, PFSC03050 *Plasmodium falciparum* DNA \*\*\* SEQUENCING... 38 4.5  
 U64827, MMU64827 *Mus musculus* extracellular matrix associated... 38 4.5  
 AC003010, HUAC003010 *Homo sapiens* Chromosome 16 BAC clone CIT... 38 4.5  
 AE001002, AE001002 *Archaeoglobus fulgidus* section 105 of 172 ... 38 4.5  
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 38 4.5  
 M20386, CHKEGFR Chicken epidermal growth factor receptor (CER... 38 4.5  
 M77637, CHKEGF *Gallus gallus* EGF/TGF-alpha receptor (c-erbB) ... 38 4.5  
 U08185, MMU08185 *Mus musculus* BALB/c zinc-finger protein Blim... 38 4.5  
 AC004231, AC004231 *Homo sapiens* chromosome 17, clone hRPC.111... 38 4.5  
 Z50100, HVC39SAT *H.vulgare* GAA-satellite DNA 38 4.5  
 X53731, SCSPA2G *S. cerevisiae* SPA2 gene 38 4.5  
 U37220, HSU37220 Human cyclophilin-like protein mRNA, partial... 38 4.5  
 X97560, SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome... 38 4.5  
 AB011479, AB011479 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5  
 U89340, LVU89340 *Lytechinus variegatus* Endo16 homolog (LvEndo1... 38 4.5  
 U73850, TCU73850 *Trypanosoma cruzi* 29 kDa proteasome subunit ... 38 4.5  
 AB006698, AB006698 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5  
 D37888, CYIMYC2 *Cyprinus carpio* c-myc gene for c-Myc, comple... 38 4.5  
 AF017349, MMDSGIII 7 *Mus musculus* desmoglein 3 (Dsg3) gene, i... 38 4.5  
 X91807, OSTA136 *O.sativa* mRNA for alpha-tubulin (clone OSTA-... 38 4.5  
 Z71587, SCYNL311C *S.cerevisiae* chromosome XIV reading frame ... 38 4.5  
 AE000742, AE000742 *Aquifex aeolicus* section 74 of 109 of the ... 38 4.5

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AA324311, AA324311 EST27136 Cerebellum II *Homo sapiens* cDNA 5... 593 e-167  
 AA639190, AA639190 ns04a01.r1 NCI\_CGAP\_Ew1 *Homo sapiens* cDNA ... 513 e-143  
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 505 e-141  
 AA588066, AA588066 nk10d08.s1 NCI\_CGAP\_Co2 *Homo sapiens* cDNA ... 502 e-140  
 AA412036, AA412036 zt68d09.s1 Soares testis NHT *Homo sapiens* ... 502 e-140  
 AA508745, AA508745 ni23a03.s1 NCI\_CGAP\_Co4 *Homo sapiens* cDNA ... 502 e-140

AA480337, AA480337 ne33a03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 502 e-140  
 AA902270, AA902270 ok69e04.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 502 e-140  
 AA947303, AA947303 ok20d04.s1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Hom... 502 e-140  
 R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136  
 AA811913, AA811913 ob51d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 464 e-128  
 AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128  
 AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109  
 R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 359 5e-97  
 AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84  
 R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68  
 AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50  
 W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20  
 W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08  
 T65784, T65784 ycl1f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14  
 AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14  
 AA928679, AA928679 on48e08.s1 NCI\_CGAP\_Co8 Homo sapiens cDNA ... 40 0.55  
 AA887972, AA887972 nq95g11.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.55  
 W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55  
 AA887862, AA887862 nq99b08.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 40 0.55  
 AA554819, AA554819 ni34d08.s1 NCI\_CGAP\_Lu1 Homo sapiens cDNA ... 40 0.55  
 AA557362, AA557362 nl81d12.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55  
 N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55  
 AA552228, AA552228 nk06b04.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 40 0.55  
 AI017648, AI017648 ou99b02.x1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 40 0.55  
 T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55  
 AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55  
 AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55  
 N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55  
 AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55  
 AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55  
 AA731625, AA731625 nw64a04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.55  
 AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55  
 AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55  
 AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55  
 R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55  
 AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55  
 AA633213, AA633213 nq57c06.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 40 0.55  
 W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55  
 AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55  
 N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55  
 N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55  
 AI041637, AI041637 ox92h08.x1 Soares\_senescent\_fibroblasts\_Nb... 40 0.55  
 N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55



AA535094, AA535094 nf84e06.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 AA514414, AA514414 nf57d11.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55  
 N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55  
 AA535811, AA535811 nf93g10.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 AA115591, AA115591 zl05g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55  
 N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55  
 AA534433, AA534433 nf80a08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55  
 AA970859, AA970859 oo81h03.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 40 0.55  
 F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55  
 AA810279, AA810279 od14g11.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.55  
 AA595146, AA595146 nl84b01.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 AA632386, AA632386 np67e06.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55  
 AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55  
 AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55  
 AA156872, AA156872 zl20h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55  
 AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55  
 AA961724, AA961724 or60a10.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 40 0.55  
 AA551210, AA551210 nj27e09.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA ... 40 0.55  
 R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55  
 AA938086, AA938086 oj08h08.s1 NCI\_CGAP\_Mel3 Homo sapiens cDNA... 40 0.55  
 AA576021, AA576021 nm57d11.s1 NCI\_CGAP\_Br3 Homo sapiens cDNA ... 40 0.55  
 AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55  
 AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55  
 T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55  
 AA632245, AA632245 np67b09.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 40 0.55  
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55  
 R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55  
 AI028447, AI028447 ow08b09.x1 Soares\_parathyroid\_tumor\_NbHPA ... 40 0.55  
 AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55  
 AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA815223, AA815223 oc05c04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.55  
 W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55  
 AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA643849, AA643849 np26f07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 40 0.55  
 AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55  
 AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55  
 AA535972, AA535972 nf95a01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 40 0.55  
 AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55  
 AA866044, AA866044 oh52g07.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.55  
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 167 1e-39  
 AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.78  
 AA413261, AA413261 ve52f04.r1 Beddington mouse embryonic regi... 38 0.78  
 AA097645, AA097645 mm36f09.r1 Stratagene mouse skin (#937313)... 38 0.78  
 AA122578, AA122578 mn25b08.r1 Beddington mouse embryonic regi... 38 0.78  
 AA122581, AA122581 mn25c08.r1 Beddington mouse embryonic regi... 38 0.78  
 AA646168, AA646168 vn11e06.r1 Stratagene mouse Tcell 937311 M... 36 3.1  
 AA200881, AA200881 mu03c09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1  
 AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 3.1  
 AA217675, AA217675 mv01b09.r1 Soares mouse lymph node NbMLN M... 36 3.1  
 AI006387, AI006387 ua71d09.r1 Soares 2NbMT Mus musculus cDNA... 36 3.1  
 AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 3.1  
 AA207387, AA207387 mv89a11.r1 GuayWoodford Beier mouse kidney... 36 3.1  
 AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 3.1  
 AA123112, AA123112 mn30g01.r1 Beddington mouse embryonic regi... 36 3.1  
 AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 3.1  
 AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 3.1  
 W12171, W12171 ma59a10.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.1  
 AA208446, AA208446 mv85e01.r1 GuayWoodford Beier mouse kidney... 36 3.1  
 AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 3.1  
 AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 3.1  
 AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 3.1  
 AA561847, AA561847 vl27a12.r1 Stratagene mouse Tcell 937311 M... 36 3.1  
 AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 3.1  
 AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1  
 AA052080, AA052080 mf69f12.r1 Soares mouse embryo NbME13.5 14... 36 3.1  
 AA000646, AA000646 mg23f09.r1 Soares mouse embryo NbME13.5 14... 36 3.1  
 AA510521, AA510521 vh59a05.r1 Soares mouse mammary gland NbMM... 36 3.1  
 AI006122, AI006122 ua86h01.r1 Soares mouse mammary gland NbMM... 36 3.1  
 AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 3.1  
 W77413, W77413 me64d06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1  
 AA114809, AA114809 mn17e09.r1 Beddington mouse embryonic regi... 36 3.1  
 AA793564, AA793564 vn54c05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.1  
 AA174537, AA174537 mt10f09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1  
 W62181, W62181 md87d08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1  
 AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.1  
 AA286005, AA286005 va30e05.r1 GuayWoodford Beier mouse kidney... 36 3.1  
 AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 3.1  
 AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 3.1

AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 44 0.011

AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 44 0.011  
 C70525, C70525 *C.elegans* cDNA clone yk409g6 : 5' end, single... 44 0.011  
 AA520235, AA520235 TgESTzz53c06.r1 TgME49 invivo Bradyzoite c... 42 0.044  
 T42800, T42800 6063 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 42 0.044  
 R29976, R29976 12581 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 42 0.044  
 H32045, H32045 EST106774 Rat PC-12 cells, untreated *Rattus* sp... 40 0.18  
 AA819924, AA819924 MF5MA171.AE3 *S. mansoni* female adult Lambd... 40 0.18  
 H37128, H37128 15257 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 40 0.18  
 T04367, T04367 414 Lambda-PRL2 *Arabidopsis thaliana* cDNA clon... 40 0.18  
 R90528, R90528 16883 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 40 0.18  
 AA660422, AA660422 00298 MtRHE *Medicago truncatula* cDNA 5' 40 0.18  
 U94861, RRU94861 *Rattus norvegicus* clone HCY3 mRNA sequence 40 0.18  
 F14275, ATTS5197 *A. thaliana* transcribed sequence; clone YBY... 38 0.69  
 W43730, W43730 23107 CD4-16 *Arabidopsis thaliana* cDNA clone H... 38 0.69  
 N65025, N65025 20065 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 38 0.69  
 AI001628, AI001628 EST0210 *Tilapia* brain cDNA library in pUC1... 38 0.69  
 H74687, H74687 383 *Brassica napus* cDNA clone R25R. 38 0.69  
 AA395597, AA395597 27394 Lambda-PRL2 *Arabidopsis thaliana* cDN... 38 0.69  
 AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.69  
 D41274, RICS3647A Rice cDNA, partial sequence (S3647\_1A). 38 0.69  
 Z25731, ATTS1208 *A. thaliana* transcribed sequence; clone VCV... 38 0.69  
 N82780, N82780 TgESTzy34e03.r1 TgRH Tachyzoite cDNA *Toxoplasma*... 38 0.69  
 AA597822, AA597822 29889 Lambda-PRL2 *Arabidopsis thaliana* cDN... 38 0.69  
 AA948906, AA948906 LD27590.5prime LD *Drosophila melanogaster* ... 38 0.69  
 AI013695, AI013695 EST208370 Normalized rat spleen, Bento Soa... 38 0.69  
 AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.69  
 F14402, ATTS5324 *A. thaliana* transcribed sequence; clone TAP... 36 2.7  
 T46158, T46158 9421 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 C91400, C91400 *Dictyostelium discoideum* slug cDNA, clone SSK169 36 2.7  
 T46009, T46009 9272 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 AA440655, AA440655 LD15510.5prime LD *Drosophila melanogaster* ... 36 2.7  
 AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A *Schistosom*... 36 2.7  
 Z32623, ATTS2751 *A. thaliana* transcribed sequence; clone YAP... 36 2.7  
 T43683, T43683 6946 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 AA263535, AA263535 LD06645.5prime LD *Drosophila melanogaster* ... 36 2.7  
 C37095, C37095 *C.elegans* cDNA clone yk482c11 : 3' end, singl... 36 2.7

C57017, C57017 *C.elegans* cDNA clone yk308h9 : 3' end, single... 36 2.7  
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 2.7  
 C92242, C92242 *Dictyostelium discoideum* slug cDNA, clone SSD283 36 2.7  
 Z33976, ATTS3037 *A. thaliana* transcribed sequence; clone YAP... 36 2.7  
 R62091, R62091 EST351 *Strongylocentrotus purpuratus* cDNA 5' end. 36 2.7  
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 2.7  
 C74456, C74456 Rice cDNA, partial sequence (E31357\_1A) 36 2.7  
 AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7  
 C92456, C92456 *Dictyostelium discoideum* slug cDNA, clone SSE569 36 2.7  
 T20458, T20458 2466 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7  
 M79841, M79841 wEST00378 *Caenorhabditis elegans* cDNA clone CE... 36 2.7  
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 2.7  
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 2.7  
 T20404, T20404 2412 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7  
 AI012789, AI012789 EST207240 Normalized rat placenta, Bento S... 36 2.7  
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 2.7  
 AA660182, AA660182 00022 *Medicago truncatula* cDNA 5' si... 36 2.7  
 D48514, RICS14740A Rice cDNA, partial sequence (S14740\_1A). 36 2.7  
 C90110, C90110 *Dictyostelium discoideum* slug cDNA, clone SSI103 36 2.7  
 H36880, H36880 15009 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7  
 AA699152, AA699152 HL07807.5prime HL *Drosophila melanogaster* ... 36 2.7  
 C11922, C11922 *C.elegans* cDNA clone yk144a11 : 5' end, singl... 36 2.7  
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 *M.musculus* mRNA for exon from unknown gene 22A3 260 5e-67  
 Z83760, CICOS41 *Ciona intestinalis* DNA sequence from cosmid ... 40 0.94  
 Z75710, CED1081 *Caenorhabditis elegans* cosmid D1081, complet... 40 0.94  
 U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94  
 X99757, DMDYDTRO *D.melanogaster* mRNA for dystrophin 38 3.7  
 U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7  
 AC004118, AC004118 *Drosophila melanogaster* (P1 DS06238 (D26))... 38 3.7  
 U50313, CELF44C4 *Caenorhabditis elegans* cosmid F44C4. 38 3.7  
 AC004503, AC004503 *Homo sapiens* chromosome 5, P1 clone 1354A7... 38 3.7  
 M16840, WHTCPA2 Wheat Asp-tRNA gene. 38 3.7  
 Y13381, RNAMPH1 *Rattus norvegicus* mRNA for amphiphysin, amph1 38 3.7  
 AC002994, AC002994 *Homo sapiens* chromosome 17, clone HRPC987K... 38 3.7  
 AB008271, AB008271 *Arabidopsis thaliana* genomic DNA, chromos... 38 3.7  
 D49701, ASNNIAD *Aspergillus oryzae* niaD gene for nitrate red... 38 3.7

X59422, HSPLD1 H.sapiens Pl d1 repetitive DNA 38 3.7  
 Z98555, PFSC03027 Plasmodium falciparum DNA \*\*\* SEQUENCING I... 38 3.7

#### HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0  
 U56653, HSU56653 Human heat shock inducible mRNA 769 0.0  
 AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0  
 AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0  
 AA314922, AA314922 EST186735 HCC cell line (matatasis to liv... 698 0.0  
 AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0  
 H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5' 624 e-177  
 AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176  
 AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170  
 AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164  
 AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150  
 AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150  
 AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150  
 AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141  
 R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5' 486 e-135  
 AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134  
 AA564849, AA564849 nj22c04.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA ... 442 e-122  
 AA932576, AA932576 oo57g10.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 440 e-121  
 AA876265, AA876265 oi12g09.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 434 e-120  
 AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118  
 U56654, HSU56654 Human heat shock inducible mRNA 426 e-117  
 AA746600, AA746600 nx18c02.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 406 e-111  
 AA876346, AA876346 oj24a11.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 406 e-111  
 W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110  
 AI034059, AI034059 ow14h11.x1 Soares parathyroid tumor NbHPA ... 357 2e-96  
 AA662934, AA662934 nu92d09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 323 2e-86  
 AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80  
 AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78  
 R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5' 280 3e-73  
 T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5' 254 2e-65  
 AA731264, AA731264 nw57c08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 220 2e-55  
 AA768549, AA768549 oa67c07.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 220 2e-55  
 AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54  
 T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3' 198 8e-49  
 AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49  
 AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22  
 R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5' 58 2e-06  
 T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5' 38 1.8  
 AA595230, AA595230 nl84g02.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 38 1.8

AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0  
 AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167  
 AI048164, AI048164 ud71b09.y1 Sugano mouse liver mlia Mus mus... 537 e-151  
 W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128  
 AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69  
 AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53  
 AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43  
 AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32  
 AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23  
 AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23  
 AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15  
 AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13  
 AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65  
 AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6  
 AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6  
 AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21  
 AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15  
 C23464, C23464 Jpanese flounder liver cDNA, LE5(10) 72 4e-11  
 C23465, C23465 Jpanese flounder liver cDNA, LE5(10) 56 2e-06  
 AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57  
 AA274286, AA274286 TgESTzz24c01.s1 TgME49 invivo Bradyzoite c... 38 0.57  
 AA660585, AA660585 00471 MtRHE Medicago truncatula cDNA 5' si... 38 0.57  
 L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57  
 AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57  
 C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3  
 C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3  
 C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3  
 AA542589, AA542589 fa08d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3  
 N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3  
 AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3  
 AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3  
 AA495181, AA495181 fa04d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3  
 D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3  
 C28238, C28238 Rice cDNA, partial sequence (C60429\_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0  
 S51239, S51239 calreticulin [*Aplysia californica*=marine snail... 56 1e-05  
 Z74035, CEF47G9 *Caenorhabditis elegans* cosmid F47G9, complet... 46 0.012  
 U25723, CPU25723 *Cavia porcellus* alpha-2B adrenoceptor gene, ... 44 0.047  
 AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19  
 U67572, U67572 *Methanococcus jannaschii* section 114 of 150 of... 42 0.19  
 V01470, ZMZE01 Zea mays gene encoding a zein gene (clone lam... 42 0.19  
 U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19  
 X82638, CSCYTOX *C.sordelii* cytotoxin gene 42 0.19  
 AE000926, AE000926 *Methanobacterium thermoautotrophicum* from ... 42 0.19  
 AC004135, AC004135 Genomic sequence for *Arabidopsis thaliana* ... 42 0.19  
 AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74  
 AF050157, MMHC135G15 *Mus musculus* major histocompatibility lo... 40 0.74  
 AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74  
 X07699, MMNUCLEO Mouse nucleolin gene 40 0.74  
 X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contai... 40 0.74  
 M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74  
 M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74  
 U15972, MMU15972 *Mus musculus* homeobox (*Hoxa7*) gene, complete... 40 0.74  
 AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74  
 U09820, HSU09820 Human helicase II (RAD54L) mRNA, complete cds. 40 0.74  
 AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74  
 U26259, MMU26259 *Mus musculus* C2-H2 zinc finger protein mRNA,... 40 0.74  
 L48363, MUSZFPTR *Mus musculus* zinc finger protein gene, compl... 40 0.74  
 AC003113, AC003113 *Arabidopsis thaliana* BAC F24O1 chromosome ... 40 0.74  
 D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74  
 U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74  
 U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74  
 U00995, U00995 *Rattus norvegicus* TA1 mRNA, complete cds. 40 0.74  
 Z48618, SCCHVII35 *S.cerevisiae* genes for RAD54, ACE1(CUP2), ... 40 0.74  
 U75653, HSU75653 Human zinc finger helicase (Znf-HX) mRNA, co... 40 0.74  
 Z72672, SCYGL150C *S.cerevisiae* chromosome VII reading frame ... 40 0.74  
 Z50109, CEC09H10 *Caenorhabditis elegans* cosmid C09H10, compl... 40 0.74  
 AF013969, AF013969 *Mus musculus* antigen containing epitope to... 40 0.74  
 M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74  
 U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74  
 M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene, c... 40 0.74  
 U76906, REU76906 *Rhizobium etli* FixK (fixK), FixN (fixN), mon... 40 0.74  
 U97085, HSXNP14 Homo sapiens X-linked nuclear protein (ATRX) ... 40 0.74  
 L34363, HUMNUCPRO Human X-linked nuclear protein (XNP) gene, ... 40 0.74  
 U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 0.74  
 U88539, MMU88539 Mus musculus chromatin structural protein ho... 40 0.74  
 U07704, HSU07704 Human protein kinase PITSLRE isoform PBETA21... 38 2.9  
 U07705, HSU07705 Human protein kinase PITSLRE isoform PBETA22... 38 2.9  
 AF019612, AF019612 Homo sapiens S2P mRNA, complete cds 38 2.9  
 U04818, HSU04818 Human protein kinase PITSLRE alpha 2-4 mRNA,... 38 2.9  
 AB002381, AB002381 Human mRNA for KIAA0383 gene, partial cds 38 2.9  
 AB009520, AB009520 Pyrococcus horikoshii OT3 genomic DNA, 13... 38 2.9  
 Z83848, HS57A13 Human DNA sequence from PAC 57A13 between ma... 38 2.9  
 AC004592, AC004592 Homo sapiens PAC clone DJ0244J05 from 5q31... 38 2.9  
 L11710, ZEFZCMYC Brachydanio rerio c-myc oncoprotein mRNA, co... 38 2.9  
 D43920, CHKMETASE Chicken mRNA for DNA (cytosine-5-)-methylt... 38 2.9  
 U49056, RNU49056 Rattus norvegicus CTD-binding SR-like protei... 38 2.9  
 U04824, HSU04824 Human protein kinase PITSLRE alpha 2-1 mRNA,... 38 2.9  
 U78045, HSU78045 Human collagenase and stromelysin genes, com... 38 2.9  
 U04816, HSU04816 Human protein kinase PITSLRE alpha 2-2 mRNA,... 38 2.9  
 U04817, HSU04817 Human protein kinase PITSLRE alpha 2-3 mRNA,... 38 2.9

#### HUMAN ESTs

AA639190, AA639190 ns04a01.r1 NCI\_CGAP\_Ew1 Homo sapiens cDNA ... 519 e-145  
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 513 e-144  
 R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136  
 AA902270, AA902270 ok69e04.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 450 e-124  
 AA947303, AA947303 ok20d04.s1 Soares NSF\_F8\_9W\_OT\_PA\_P\_S1 Hom... 402 e-110  
 AA588066, AA588066 nk10d08.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA ... 347 1e-93  
 AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 347 1e-93  
 AA480337, AA480337 ne33a03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 347 1e-93  
 AA508745, AA508745 ni23a03.s1 NCI\_CGAP\_Co4 Homo sapiens cDNA ... 347 1e-93  
 AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 315 4e-84  
 AA811913, AA811913 ob51d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 299 2e-79  
 AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 299 2e-79  
 AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 250 2e-64  
 R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 250 2e-64  
 W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 3e-20  
 W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 6e-09  
 AA737681, AA737681 nw63c04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 42 0.090  
 T65784, T65784 ycl1f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.090  
 R52021, R52021 yg84h09.r1 Homo sapiens cDNA clone 40181 5' si... 42 0.090  
 AA569993, AA569993 nm47h04.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 42 0.090  
 R50149, R50149 yj61c05.s1 Homo sapiens cDNA clone 153224 3' s... 42 0.090  
 R87930, R87930 yo47a11.s1 Homo sapiens cDNA clone 181052 3' s... 42 0.090  
 AA812204, AA812204 ob84f01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 42 0.090  
 AA770224, AA770224 ah82e12.s1 Soares testis NHT Homo sapiens ... 42 0.090



D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36  
 AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36  
 AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36  
 T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36  
 AA974278, AA974278 oq14d03.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.36  
 W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36  
 H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36  
 AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36  
 N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36  
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36  
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36  
 H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36  
 AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36  
 W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36  
 T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36  
 AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4  
 AA993061, AA993061 ot92h08.s1 Soares\_total\_fetus\_Nb2HF8\_9w Ho... 38 1.4  
 R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4  
 H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4  
 W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4  
 N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4  
 AA630851, AA630851 nt57f04.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA ... 38 1.4  
 N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4  
 AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4  
 AA911761, AA911761 og19b01.s1 NCI\_CGAP\_PNS1 Homo sapiens cDNA... 38 1.4  
 AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4  
 AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4  
 AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4  
 F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4  
 AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4  
 AA908705, AA908705 ol01b09.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 38 1.4  
 AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41  
 AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032  
 AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032  
 AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13  
 AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13  
 AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13  
 AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13  
 AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13  
 AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037 vc68g03.s1 Knowles Solter mouse 2 cell Mus... 40 0.13  
 AA596585, AA596585 vm58e12.r1 Stratagene mouse Tcell 937311 M... 38 0.51  
 AA863563, AA863563 vx05a10.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.51  
 AA795177, AA795177 vq94g04.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA914764, AA914764 vy92h04.r1 Soares mouse mammary gland NbMM... 38 0.51  
 AA590440, AA590440 vm20c04.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA260352, AA260352 va93c10.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.51  
 AA444734, AA444734 ve75d10.r1 Soares mouse mammary gland NbMM... 38 0.51  
 C85885, C85885 Mus musculus fertilized egg cDNA 3'-end seque... 38 0.51  
 AA794590, AA794590 vu78h12.r1 Stratagene mouse skin (#937313)... 38 0.51  
 AA529643, AA529643 vi38a09.r1 Beddington mouse embryonic regi... 38 0.51  
 AA607084, AA607084 vm84a09.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA636994, AA636994 vn05g06.r1 Knowles Solter mouse blastocyst... 38 0.51  
 AA675676, AA675676 vr73h08.s1 Knowles Solter mouse 2 cell Mus... 38 0.51  
 AA163890, AA163890 ms52f09.r1 Life Tech mouse embryo 13 5dpc ... 38 0.51  
 C80539, C80539 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 38 0.51  
 AA051352, AA051352 mj53a09.r1 Soares mouse embryo NbME13.5 14... 38 0.51  
 W36885, W36885 mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus... 38 0.51  
 AA930627, AA930627 vy67c05.r1 Stratagene mouse macrophage (#9... 38 0.51  
 AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 2.0  
 AA967267, AA967267 vz70e08.r1 Soares mouse mammary gland NbMM... 36 2.0  
 AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 2.0  
 AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 2.0  
 AA170036, AA170036 ms52d01.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0  
 AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 2.0  
 AA555634, AA555634 vk49f08.r1 Stratagene mouse Tcell 937311 M... 36 2.0  
 AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 2.0  
 AA606813, AA606813 vm90h12.r1 Knowles Solter mouse blastocyst... 36 2.0  
 AA591610, AA591610 vk49d08.r1 Stratagene mouse Tcell 937311 M... 36 2.0  
 AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 2.0  
 AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 2.0  
 AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 2.0  
 AA612185, AA612185 vo03d05.r1 Stratagene mouse skin (#937313)... 36 2.0  
 AA103424, AA103424 mo21e05.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0  
 AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.0  
 AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.0  
 AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 2.0  
 AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 2.0  
 AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 2.0  
 AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 2.0  
 AA655241, AA655241 vq84c07.s1 Knowles Solter mouse 2 cell Mus... 36 2.0  
 AA512835, AA512835 vg13f11.r1 Soares mouse NbMH Mus musculus ... 36 2.0

C70525, C70525 *C.elegans* cDNA clone yk409g6 : 5' end, single... 44 0.007  
 F15112, SSO4D09 *S.scrofa* mRNA; expressed sequence tag (5'; c... 42 0.029  
 AA684640, AA684640 EST104989 Rat PC-12 cells, untreated Rattu... 40 0.11  
 H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.11  
 AA660422, AA660422 00298 *MtRHE* *Medicago truncatula* cDNA 5' 40 0.11  
 C59696, C59696 *C.elegans* cDNA clone yk440e1 : 3' end, single... 38 0.45  
 AI008699, AI008699 EST203150 Normalized rat embryo, Bento Soa... 38 0.45  
 AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.45  
 T38461, T38461 EST103957 *Saccharomyces cerevisiae* cDNA 3' end. 38 0.45  
 C59257, C59257 *C.elegans* cDNA clone yk386b12 : 3' end, singl... 38 0.45  
 AA948906, AA948906 LD27590.5prime LD *Drosophila melanogaster* ... 38 0.45  
 AI001628, AI001628 EST0210 *Tilapia* brain cDNA library in pUC1... 38 0.45  
 H31962, H31962 EST106545 Rat PC-12 cells, untreated Rattus sp... 38 0.45  
 AA979509, AA979509 LD34118.5prime LD *Drosophila melanogaster* ... 38 0.45  
 D41274, RICS3647A Rice cDNA, partial sequence (S3647\_1A). 38 0.45  
 C58362, C58362 *C.elegans* cDNA clone yk366a8 : 3' end, single... 38 0.45  
 C57756, C57756 *C.elegans* cDNA clone yk298b9 : 3' end, single... 38 0.45  
 AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.45  
 H74687, H74687 383 *Brassica napus* cDNA clone R25R. 38 0.45  
 C10513, C10513 *C.elegans* cDNA clone yk147e9 : 3' end, single... 38 0.45  
 C55569, C55569 *C.elegans* cDNA clone yk191d1 : 3' end, single... 38 0.45  
 C94819, C94819 *Sus scrofa* mRNA; expressed sequence tag (5'; ... 38 0.45  
 C32982, C32982 *C.elegans* cDNA clone yk338a12 : 3' end, singl... 38 0.45  
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 1.8  
 AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA660182, AA660182 00022 *MtRHE* *Medicago truncatula* cDNA 5' si... 36 1.8  
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 1.8  
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 1.8  
 AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 1.8  
 AA440655, AA440655 LD15510.5prime LD *Drosophila melanogaster* ... 36 1.8  
 AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A *Schistosom*... 36 1.8  
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 1.8  
 AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 T46158, T46158 9421 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 1.8  
 AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 1.8  
 AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 1.8  
 AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 36 1.8  
 C37095, C37095 *C.elegans* cDNA clone yk482c11 : 3' end, singl... 36 1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8  
 T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8  
 F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8  
 T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8  
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8  
 AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8  
 AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

## SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092  
 U50719, MSU50719 Manduca sexta neuroglial mRNA, complete cds 40 0.36  
 Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36  
 AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36  
 X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36  
 D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36  
 AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4  
 AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4  
 X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene 38 1.4  
 X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

## HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0  
 D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0  
 D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0  
 H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172  
 AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166  
 AA977877, AA977877 oq56d03.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 571 e-161  
 AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159  
 AA972542, AA972542 oo82e01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 561 e-158  
 AA954270, AA954270 on72e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 557 e-157  
 AA740333, AA740333 ob23c02.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 557 e-157  
 AA999722, AA999722 ov04c06.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 555 e-156  
 AA970621, AA970621 op40h08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 551 e-155  
 AA932930, AA932930 oo04g11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 541 e-152  
 AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152  
 W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152  
 AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152  
 R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3' s... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150  
AI027967, AI027967 ov84d04.x1 Soares\_testis\_NHT Homo sapiens ... 535 e-150  
AA776717, AA776717 ah49d07.s1 Soares\_testis\_NHT Homo sapiens ... 535 e-150  
AI040961, AI040961 ov53d06.x1 Soares\_testis\_NHT Homo sapiens ... 533 e-150  
AI024835, AI024835 ov35h09.x1 Soares\_testis\_NHT Homo sapiens ... 533 e-150  
AA740667, AA740667 ob01g12.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 531 e-149  
AA994527, AA994527 ou42h06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 531 e-149  
AA932728, AA932728 oo31g06.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 529 e-149  
AI001978, AI001978 ot39f03.s1 Soares\_testis\_NHT Homo sapiens ... 529 e-149  
N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149  
N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148  
AA883578, AA883578 al46b08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 527 e-148  
AA890154, AA890154 al53f07.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 525 e-147  
AA757222, AA757222 ah56f11.s1 Soares\_testis\_NHT Homo sapiens ... 525 e-147  
AA456074, AA456074 aa17b07.s1 Soares\_NhHMPu\_S1 Homo sapiens c... 523 e-147  
AA884285, AA884285 am32f04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 523 e-147  
AA969436, AA969436 op53e12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 521 e-146  
AA952918, AA952918 on55h11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 521 e-146  
AA971938, AA971938 op88b01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 521 e-146  
R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146  
AA865258, AA865258 og87d08.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 519 e-146  
AA758323, AA758323 ah65e11.s1 Soares\_testis\_NHT Homo sapiens ... 519 e-146  
AA972041, AA972041 op88e06.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 519 e-146  
R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146  
AA917965, AA917965 om37e04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 517 e-145  
AA505880, AA505880 ni01a09.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 517 e-145  
AA906270, AA906270 oj98e12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 517 e-145  
AA758549, AA758549 ah70b04.s1 Soares\_testis\_NHT Homo sapiens ... 517 e-145  
AA927156, AA927156 om20f05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 515 e-144  
AA976254, AA976254 oo30f08.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 515 e-144  
R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144  
AA938552, AA938552 oo78g11.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 513 e-144  
AA483809, AA483809 ne41c08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 513 e-144  
AA962659, AA962659 or31f10.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA ... 511 e-143  
AA724803, AA724803 ai05f02.s1 Soares\_parathyroid\_tumor\_NbHPA ... 511 e-143  
AA410432, AA410432 zv12c09.s1 Soares\_NhHMPu\_S1 Homo sapiens c... 511 e-143  
AA775373, AA775373 ad19c07.s1 Soares\_NbHFB Homo sapiens cDNA ... 511 e-143  
AA758038, AA758038 ah67h09.s1 Soares\_testis\_NHT Homo sapiens ... 509 e-143  
AA904368, AA904368 ol15d02.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 509 e-143  
AA861386, AA861386 ak37b11.s1 Soares\_testis\_NHT Homo sapiens ... 507 e-142  
R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141  
AA843421, AA843421 ak07f11.s1 Soares\_parathyroid\_tumor\_NbHPA ... 504 e-141  
H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141  
N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141  
AA815351, AA815351 ai63g05.s1 Soares\_testis\_NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 502 e-140  
H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140  
AA988977, AA988977 or87e11.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 500 e-140  
AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140  
AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139  
AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139  
R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139  
H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139  
AA875917, AA875917 oj15a08.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 496 e-138  
R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138  
AA970616, AA970616 op40h03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 494 e-138  
AA912408, AA912408 ol23a05.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 492 e-137  
AA910051, AA910051 ol40e08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 492 e-137  
AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137  
R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136  
AA954722, AA954722 oo84c12.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 488 e-136  
R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136  
R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136  
AA885425, AA885425 am12h09.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 486 e-136  
AA884231, AA884231 am32a01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 484 e-135  
AA885048, AA885048 am11a12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 482 e-134  
AA996162, AA996162 os14f10.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 482 e-134  
AA748637, AA748637 ny10a02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 482 e-134  
AI031908, AI031908 ow47e12.x1 Soares\_parathyroid\_tumor\_NbHPA ... 482 e-134  
AA884703, AA884703 am18e02.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 480 e-134  
AA928243, AA928243 on87c10.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 480 e-134  
AI025986, AI025986 ow03a09.s1 Soares\_parathyroid\_tumor\_NbHPA ... 478 e-133  
AA897637, AA897637 oj72g07.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 472 e-131  
AA877346, AA877346 olc07.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 472 e-131  
AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131  
AA832163, AA832163 oc91b02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 470 e-131  
R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131  
N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128  
R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126  
AA579968, AA579968 ng51c03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 444 e-123  
AA843427, AA843427 ak07g06.s1 Soares\_parathyroid\_tumor\_NbHPA ... 438 e-121  
AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121  
AA835882, AA835882 oc81d05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 434 e-120  
AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119  
AA512970, AA512970 nj16b08.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 432 e-119  
R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118  
AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114  
H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111  
AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110  
AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103  
 AA577436, AA577436 nm96h06.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 351 4e-95  
 AA516390, AA516390 nf55e03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 347 6e-94  
 AA534533, AA534533 nf80h06.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 341 3e-92  
 AA541583, AA541583 ni89f05.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 311 3e-83  
 N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3'. 303 8e-81  
 AA905015, AA905015 ok09b08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 303 8e-81  
 AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76  
 AA939048, AA939048 op56h04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 256 2e-66  
 AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63  
 R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61  
 AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59  
 W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44  
 AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44  
 AA455577, AA455577 aal7b07.r1 Soares\_NhHMPu S1 Homo sapiens c... 176 1e-42  
 AA583931, AA583931 nn64e04.s1 NCI\_CGAP\_Lar1 Homo sapiens cDNA... 172 2e-41  
 AA907332, AA907332 ol22g11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 168 3e-40  
 R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37  
 W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36  
 AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30  
 AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19  
 H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19  
 AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18  
 AA931370, AA931370 oo03d01.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapien... 96 3e-18  
 AA501911, AA501911 ng54a08.s1 NCI\_CGAP\_Li2 Homo sapiens cDNA ... 94 1e-17  
 AA548419, AA548419 nj14g09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 92 5e-17  
 AA588892, AA588892 no23b06.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 92 5e-17  
 AI025228, AI025228 ov40h08.x1 Soares testis NHT Homo sapiens ... 76 3e-12  
 R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11  
 R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06  
 N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04  
 H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04  
 H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011  
 N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70  
 AA614692, AA614692 np52b10.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDN... 38 0.70  
 H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7  
 H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7  
 AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7  
 AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7  
 AA632009, AA632009 np74c07.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 36 2.7  
 H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7  
 AI022018, AI022018 ow64d01.x1 Soares\_senescent\_fibroblasts\_Nb... 36 2.7  
 AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7  
 N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7  
 AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65  
 AA051612, AA051612 mj52c07.r1 Soares mouse embryo NbME13.5 14... 238 1e-61  
 AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst... 234 2e-60  
 AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56  
 AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56  
 AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54  
 AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50  
 W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48  
 AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34  
 W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27  
 Z31174, MMTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25  
 AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12  
 AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11  
 AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004  
 AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99  
 AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99  
 AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99  
 AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99  
 W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99  
 AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99  
 AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99  
 Z31139, MMTEST427 M.musculus expressed sequence tag MTEST427 36 0.99  
 C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9  
 AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9  
 AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9  
 W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9  
 AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9  
 AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9  
 AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9  
 AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9  
 AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9  
 AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9  
 AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9  
 W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9  
 AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9  
 AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9



AI043768, AI043768 UI-R-C0-jm-d-11-0-UI.s1 UI-R-C0 Rattus nor... 174 1e-42  
 AA531635, AA531635 TgESTzz29b08.r1 TgME49 invivo Bradyzoite c... 38 0.22  
 AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22  
 AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87  
 D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87  
 AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87  
 AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5  
 C20118, C20118 Rice cDNA, partial sequence (E11542\_2A) 34 3.5  
 AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5  
 AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

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U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11  
 V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45  
 X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45  
 U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8  
 U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8  
 U04101, POU04101 Pleurotus ostreatus D1742, Japan, mating gro... 38 1.8  
 AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8  
 M18680, HUMRGAPS Homo sapiens 5S rRNA pseudogene. 38 1.8  
 AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8  
 AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8  
 Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8  
 U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8  
 U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8  
 U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8  
 U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8  
 U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

# HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147  
 AA834501, AA834501 of21c02.s1 NCI\_CGAP\_Kid6 Homo sapiens cDNA... 381 e-104  
 W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84  
 R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54  
 AA761660, AA761660 nz24b09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 212 3e-53  
 AA887861, AA887861 nq99b07.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 74 2e-11  
 AA644044, AA644044 nm20b12.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22  
AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22  
T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86  
AA515882, AA515882 nf67f10.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 38 0.86  
AA664812, AA664812 nu69b05.s1 NCI\_CGAP\_Alv1 Homo sapiens cDNA... 36 3.4  
T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4  
AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4  
AA916894, AA916894 og34g10.s1 NCI\_CGAP\_Br7 Homo sapiens cDNA ... 36 3.4  
N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4  
AA953544, AA953544 om79g06.s1 NCI\_CGAP\_Kid3 Homo sapiens cDNA... 36 3.4  
AA505576, AA505576 nh93f03.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 36 3.4  
H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4  
AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4  
AA595583, AA595583 nk92c04.s1 NCI\_CGAP\_Co11 Homo sapiens cDNA... 36 3.4  
AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4  
AA810167, AA810167 ob88a03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 36 3.4  
H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4  
W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4  
R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4  
AA514234, AA514234 nf56e10.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms  
AA821640, AA821640 vw  
AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001  
T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069  
AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1  
AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1  
AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1  
AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3  
R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3  
AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

SEQ ID NO:560

X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

Z50028, X72735, U13072, Z34294, AB002109, X68401, M92840, D88399, Z36238, AF000262, Z46828,

# HUMAN ESTs

AA215808, AA215808 zr98b10.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 1082 0.0  
 N75131, N75131 yz29g07.r1 Soares multiple sclerosis 2NbHMSP H... 989 0.0  
 AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0  
 AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0  
 AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0  
 AA878521, AA878521 oj19c01.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA... 844 0.0  
 AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0  
 W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0  
 AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0  
 N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0  
 N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0  
 AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0  
 AA768023, AA768023 oa60e03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 728 0.0  
 AA872018, AA872018 oi05f08.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 718 0.0  
 AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0  
 AA814881, AA814881 oa75e02.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 708 0.0  
 R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0  
 W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0  
 R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0  
 D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10. 630 e-179  
 AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178  
 AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177  
 R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176  
 AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175  
 AA633335, AA633335 nq58h09.s1 NCI\_CGAP\_Co9 Homo sapiens cDNA ... 611 e-173  
 AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169  
 R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168  
 AA872617, AA872617 oi05g07.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 591 e-167  
 H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166  
 AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159  
 H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153  
 AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147  
 AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145  
 AA297001, AA297001 EST112550 Adipose tissue, white II Homo sa... 502 e-140  
 AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139  
 AA769090, AA769090 oa74e12.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 494 e-138  
 H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121  
 H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120  
 AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116  
 D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113  
 AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102  
 AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101  
 AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101  
 AA932620, AA932620 oo61h04.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 365 4e-99  
 AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91  
 AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76  
 AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71  
 H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66  
 R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66  
 AA229414, AA229414 nc47f12.r1 NCI\_CGAP\_Pr3 Homo sapiens cDNA ... 246 3e-63  
 D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52  
 AA249061, AA249061 ll4438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40  
 R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33  
 R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19  
 AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081  
 AA977111, AA977111 oq24c03.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 40 0.32  
 AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0  
 gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0  
 gb|AA510881|AA510881 vh59c11.r1 Soares mouse mammary gland NbMM... 617 e-175  
 gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174  
 gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155  
 gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153  
 gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123  
 gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117  
 gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108  
 emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83  
 gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78  
 gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76  
 gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69  
 gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69  
 gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62  
 dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41  
 gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19  
 gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12  
 gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08  
 gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06  
 gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04  
 gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45  
 gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8  
 gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8  
  
 gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161  
 gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108  
 gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96  
 gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90  
 gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82  
 gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82  
 gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73  
 gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37  
 gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34  
 dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10  
 gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6  
 dbj|C22690|C22690 Rice cDNA, partial sequence (S5274\_4A) 36 1.6  
 gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6  
 gb|AA550136|AA550136 1244m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 1.6  
 gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6  
 gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6  
 gb|AA056876|AA056876 SWMFCA987SK Brugia malayi microfilaria cDN... 36 1.6  
 gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

## SEQ ID NO:561

emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10  
 gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10  
 emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10  
 gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10  
 gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10  
 dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40  
 dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40  
 gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40  
 emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6  
 dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6  
 gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6  
 emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6  
 gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

## HUMAN ESTs

gb|AA401219|AA401219 zv63a03.r1 Soares total fetus Nb2HF8 9w Ho... 993 0.0  
 gb|H69371|H69371 yu19h09.r1 Homo sapiens cDNA clone 234305 5' s... 44 0.049  
 gb|N62576|N62576 za13d10.s1 Homo sapiens cDNA clone 292435 3' s... 42 0.19  
 gb|W77763|W77763 zd69c06.r1 Soares fetal heart NbHH19W Homo sap... 40 0.77  
 gb|R14832|R14832 yf93g05.r1 Homo sapiens cDNA clone 30203 5'. 40 0.77  
 gb|T90524|T90524 yd40a04.s1 Homo sapiens cDNA clone 110670 3' s... 38 3.0  
 gb|R91887|R91887 yq04c09.r1 Homo sapiens cDNA clone 195952 5'. 38 3.0  
 gb|AA586935|AA586935 nn68h03.s1 NCI\_CGAP\_Lar1 Homo sapiens cDNA... 38 3.0  
 gb|T46987|T46987 yb12a07.s1 Homo sapiens cDNA clone 70932 3' co... 38 3.0  
 gb|AA853975|AA853975 aj51f09.s1 Soares testis NHT Homo sapiens ... 38 3.0  
 gb|T97059|T97059 ye50e01.r1 Homo sapiens cDNA clone 121176 5'. 38 3.0  
 gb|AA883119|AA883119 am15h02.s1 Soares NFL T GBC S1 Homo sapien... 38 3.0  
 gb|AA860074|AA860074 ak45b06.s1 Soares testis NHT Homo sapiens ... 38 3.0  
 gb|AA889618|AA889618 ak28f06.s1 Soares\_testis\_NHT Homo sapiens ... 38 3.0

gb|AA230450|AA230450 mv73c06.r1 Soares mouse 3NME12 5 Mus muscu... 38 1.1  
 gb|AA058041|AA058041 mj58e08.r1 Soares mouse embryo NbME13.5 14... 38 1.1  
 gb|AA152953|AA152953 mq54a03.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1  
 gb|W34414|W34414 ma98b07.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.1  
 gb|AA465969|AA465969 ve90c06.s1 Knowles Solter mouse 2 cell Mus... 38 1.1  
 gb|AA261173|AA261173 mz62b11.r1 Soares mouse lymph node NbMLN M... 38 1.1  
 gb|AA238109|AA238109 mw97b05.r1 Soares mouse NML Mus musculus c... 38 1.1  
 dbj|C86549|C86549 Mus musculus fertilized egg cDNA 3'-end seque... 38 1.1  
 gb|AI048677|AI048677 ub29g09.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1  
 dbj|D77921|MUSC1A08 Mouse embryonal carcinoma F9 cell cDNA, C1A08 38 1.1  
 gb|AA396183|AA396183 vb45e04.r1 Soares mouse lymph node NbMLN M... 38 1.1  
 gb|AA465898|AA465898 vc62f12.s1 Knowles Solter mouse 2 cell Mus... 36 4.3  
 gb|AA041869|AA041869 mj05b12.r1 Soares mouse embryo NbME13.5 14... 36 4.3  
 gb|AA637824|AA637824 vr21f11.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3  
 gb|W82563|W82563 mf05g06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.3  
 gb|AA389972|AA389972 vb30e03.r1 Soares mouse lymph node NbMLN M... 36 4.3  
 gb|AA396253|AA396253 vb45f08.r1 Soares mouse lymph node NbMLN M... 36 4.3  
 gb|AA920907|AA920907 vy84f04.r1 Stratagene mouse macrophage (#9... 36 4.3  
 gb|AA517166|AA517166 vh98h05.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3  
 gb|AA433599|AA433599 vf47a05.r1 Soares mouse NbMH Mus musculus ... 36 4.3  
 gb|AA867252|AA867252 vx25c01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.3  
 dbj|C85619|C85619 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.3  
 gb|AA260277|AA260277 va93g05.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.3  
 gb|AA172548|AA172548 mt04g11.r1 Soares mouse 3NbMS Mus musculus... 36 4.3  
 gb|AA266879|AA266879 mz96a02.r1 Soares mouse lymph node NbMLN M... 36 4.3  
 gb|AA473019|AA473019 vd43e06.r1 Barstead MPLRB1 Mus musculus cD... 36 4.3

gb|R47549|R47549 SW3ICA119SK *Brugia malayi* infective larva cDNA... 40 0.24  
 gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated *Rattus* sp... 38 0.96  
 gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 *Rattus* nor... 38 0.96  
 gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 *Rattus* nor... 38 0.96  
 gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96  
 gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96  
 gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96  
 gb|R95272|R95272 SWOvL3CA167SK *Onchocerca volvulus* infective la... 36 3.8  
 gb|AA917208|AA917208 ka05f02.s1 *Onchocerca volvulus* infective l... 36 3.8  
 dbj|C62023|C62023 *C.elegans* cDNA clone yk249d5 : 5' end, single... 36 3.8  
 gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8  
 gb|AI043280|AI043280 TENU0920 *T. cruzi* epimastigote normalized ... 36 3.8  
 gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8  
 gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8  
 dbj|C62878|C62878 *C.elegans* cDNA clone yk296d4 : 5' end, single... 36 3.8  
 gb|AA915818|AA915818 SWOvL3CA1269SK *Onchocerca volvulus* infecti... 36 3.8  
 gb|W00009|W00009 TgESTzy75b07.r1 TgRH Tachyzoite cDNA *Toxoplasma*... 36 3.8  
 gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8  
 gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 *Rattus* nor... 36 3.8  
 gb|H54977|H54977 HHU16a *Sorghum bicolor* cv. TX430 *Sorghum bicol*... 36 3.8

## SEQ ID NO:562

gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082  
 gb|U50197|CELF25E2 *Caenorhabditis elegans* cosmid F25E2. 44 0.082  
 dbj|AB007727|AB007727 *Arabidopsis thaliana* genomic DNA, chromos... 44 0.082  
 gb|U02562|BSU02562 *Bacillus subtilis* N-acetylglucosaminidase (l... 42 0.32  
 dbj|D45048|BACORFX *Bacillus subtilis* gene for beta-N-acetylgluc... 42 0.32  
 emb|Z70683|CEF13B12 *Caenorhabditis elegans* cosmid F13B12, compl... 40 1.3  
 emb|AL023828|CEY17G7B *Caenorhabditis elegans* cosmid Y17G7B, com... 40 1.3  
 gb|U39740|CELZC64 *Caenorhabditis elegans* cosmid ZC64. 40 1.3  
 gb|AF006490|AF006490 *Gossypium hirsutum* adenine nucleotide tran... 40 1.3  
 emb|AL010170|PFSC03098 *Plasmodium falciparum* DNA \*\*\* SEQUENCING... 40 1.3  
 gb|U53701|GHU53701 *Gossypium hirsutum* alcohol dehydrogenase 2d ... 40 1.3

## HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0  
 gb|AA251062|AA251062 zs07c10.r1 NCI\_CGAP\_GCB1 *Homo sapiens* cDNA... 795 0.0

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0  
 gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165  
 gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154  
 gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148  
 gb|AA225705|AA225705 nc10b05.r1 NCI\_CGAP\_Pr1 Homo sapiens cDNA ... 515 e-144  
 gb|W27883|W27883 39b10 Human retina cDNA randomly primed sublib... 484 e-134  
 gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121  
 gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119  
 gb|AA250933|AA250933 zs07d01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 426 e-117  
 gb|AA216370|AA216370 nc10b05.s1 NCI\_CGAP\_Pr1 Homo sapiens cDNA ... 398 e-109  
 gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108  
 gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108  
 gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97  
 gb|AA602297|AA602297 np25a11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 281 1e-73  
 gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66  
 gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59  
 gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56  
 gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55  
 dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47  
 gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38  
 gb|AA642960|AA642960 60f07.s1 NCI\_CGAP\_Lym3 Homo sapiens cDNA... 147 4e-33  
 gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62  
 gb|AA521500|AA521500 aa73h08.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 40 0.62  
 gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62  
 gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4  
 dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4  
 gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104  
 gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93  
 gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60  
 gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60  
 gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44  
 gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05  
 gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001  
 gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001  
 gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001  
 gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001  
 gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001  
 gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004  
 gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056



gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88  
gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88  
dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88  
gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88  
gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88  
gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5  
gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5  
gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5  
gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5  
emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5  
gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5  
gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5  
gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5  
gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5  
gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78  
gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78  
gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78  
gb|H33464|H33464 EST109494 Rat PC-12 cells, NGF-treated (9 days... 38 0.78  
gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1  
dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1  
gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1  
gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1  
gb|N60251|N60251 TgESTzy11d04.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 3.1  
gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1  
gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1  
gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1  
gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1  
gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1  
gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

SEQ ID NO:563

substantially identical to D86956

SEQ ID NO:564

gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41  
 gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23  
 gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23  
 gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23  
 gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22  
 emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21  
 gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19  
 gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17  
 gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15  
 gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14  
 gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13  
 gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13  
 emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13  
 emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12  
 gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12  
 gb|G29058|G29058 chicken STS ADL368 76 3e-11  
 gb|G29060|G29060 chicken STS ADL352 76 3e-11  
 gb|U34048|H DU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11  
 gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09  
 gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08  
 gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06  
 gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06  
 emb|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06  
 gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029  
 emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12  
 emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12  
 gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46  
 emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46  
 emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46  
 emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46  
 gb|L13767|STMSEC101A Streptomyces lividans sec101 gene, 5' end p... 42 0.46  
 emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8  
 gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 gb|J02871|HUMCP45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8  
 dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8  
 gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8  
 gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8  
 emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8  
 gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8  
 emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8  
 gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

## HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0  
 gb|AA975279|AA975279 oq36e08.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA ... 900 0.0  
 gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0  
 gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0  
 gb|AA632259|AA632259 np67d04.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA ... 730 0.0  
 gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0  
 gb|AA515175|AA515175 ng68f10.s1 NCI\_CGAP\_Lip2 Homo sapiens cDNA... 615 e-174  
 gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172  
 gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165  
 gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165  
 gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163  
 gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163  
 gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157  
 gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149  
 gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147  
 gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139  
 gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134  
 gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129  
 gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125  
 gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115  
 gb|AA907095|AA907095 ol03b12.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA ... 414 e-113  
 gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67  
 gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55  
 gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55  
 gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52  
 gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47  
 gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24  
 N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109  
 gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105  
 gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93  
 gb|AA028696|AA028696 mi12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82  
 gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62  
 gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57  
 gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57  
 dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57  
 gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17  
 gb|AA667535|AA667535 vv18b12.r1 Stratagene mouse heart (#937316... 40 0.31  
 gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb|AA444814|AA444814 vg50e04.r1 Soares mouse mammary gland NbMM... 38 1.2  
 gb|AA763341|AA763341 vw53b12.r1 Soares mouse mammary gland NMLM... 38 1.2  
 gb|AA110827|AA110827 mp57a12.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2  
 gb|AA691932|AA691932 vt06b04.r1 Barstead mouse myotubes MPLRB5 ... 38 1.2  
 gb|W77233|W77233 me61f11.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2  
 gb|AA072872|AA072872 mm80g08.r1 Stratagene mouse embryonic carc... 38 1.2  
 gb|AA980630|AA980630 ua43f05.r1 Soares mouse mammary gland NbMM... 36 4.9  
 gb|AA065522|AA065522 ml54d09.r1 Stratagene mouse testis (#93730... 36 4.9  
 gb|AA982398|AA982398 uh07b08.r1 Soares mouse hypothalamus NMHy ... 36 4.9  
 gb|W62610|W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9  
 gb|AA286651|AA286651 vb79b02.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.9  
 gb|AA399772|AA399772 vd70g05.r1 Beddington mouse embryonic regi... 36 4.9  
 gb|AA510475|AA510475 vg32h08.r1 Soares mouse mammary gland NbMM... 36 4.9  
 gb|AA109064|AA109064 ml63g02.r1 Stratagene mouse testis (#93730... 36 4.9  
 gb|AA033485|AA033485 mi42c08.r1 Soares mouse embryo NbME13.5 14... 36 4.9  
 gb|W57221|W57221 md59g10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9  
 gb|AA467106|AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 36 4.9  
 gb|W97470|W97470 mf95a11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9  
 gb|AA606917|AA606917 vm91c05.r1 Knowles Solter mouse blastocyst... 36 4.9  
 dbj|C78330|C78330 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9  
 gb|AA013753|AA013753 mh26h12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9  
 gb|AA145240|AA145240 mr12a03.r1 Soares mouse 3NbMS Mus musculus... 36 4.9  
 gb|AA245533|AA245533 mx03c11.r1 Soares mouse NML Mus musculus c... 36 4.9  
 gb|AA770893|AA770893 vt13a08.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9  
 dbj|C79987|C79987 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9  
 gb|AA014027|AA014027 mh24a12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9  
 dbj|C89051|C89051 Mus musculus early blastocyst cDNA, clone 01B... 36 4.9  
 gb|AA058308|AA058308 mj59e09.r1 Soares mouse embryo NbME13.5 14... 36 4.9  
 gb|AA673826|AA673826 vu08h10.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9  
 gb|AA637080|AA637080 vn07h04.r1 Knowles Solter mouse blastocyst... 36 4.9  
 gb|W44292|W44292 mc80c07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9

gb|AA955972|AA955972 UI-R-E1-ff-d-10-0-UI.s1 UI-R-E1 Rattus nor... 159 4e-37  
 gb|AA957275|AA957275 UI-R-E1-fq-f-08-0-UI.s1 UI-R-E1 Rattus nor... 157 2e-36  
 emb|Z84031|SSZ84031 S.scrofa mRNA; expressed sequence tag (5'; ... 111 9e-23  
 gb|AF041408|AF041408 Fragaria x ananassa clone FA110b 96 5e-18  
 gb|AA933116|AA933116 SWBmL3SA048T3 Brugia malayi L3 subtracted ... 58 1e-06  
 gb|AA933363|AA933363 SWBmL3SA615T3 Brugia malayi L3 subtracted ... 52 7e-05  
 gb|AA660164|AA660164 00001 MirHE Medicago truncatula cDNA 5' si... 50 3e-04  
 gb|N37420|N37420 18647 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018  
 gb|H35981|H35981 14503 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018  
 gb|AA882627|AA882627 TENS0198 T. cruzi epimastigote normalized ... 44 0.018  
 gb|AI026481|AI026481 TENU0693 T. cruzi epimastigote normalized ... 42 0.070  
 gb|AA946369|AA946369 EST201868 Normalized rat lung, Bento Soare... 42 0.070

gb|AI010371|AI010371 EST204822 Normalized rat lung, Bento Soare... 42 0.070  
 gb|AI010257|AI010257 EST204708 Normalized rat lung, Bento Soare... 42 0.070  
 dbj|D39318|RICR3325A Rice cDNA, partial sequence (R3325\_1A). 40 0.28  
 gb|U40140|OSU40140 Oryza sativa clone pFDRRC22 mRNA sequence. 40 0.28  
 gb|AI009132|AI009132 EST203583 Normalized rat embryo, Bento Soa... 40 0.28  
 dbj|D47291|RICS12574A Rice cDNA, partial sequence (S12574\_1A). 40 0.28  
 dbj|D47316|RICS12613A Rice cDNA, partial sequence (S12613\_1A). 40 0.28  
 gb|T42265|T42265 5528 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 40 0.28  
 dbj|D47631|RICS13239A Rice cDNA, partial sequence (S13239\_1A). 40 0.28  
 gb|AI013513|AI013513 EST208188 Normalized rat spleen, Bento Soa... 40 0.28  
 gb|AA751980|AA751980 96AS0896 Rice Immature Seed Lambda ZAPII c... 40 0.28  
 gb|AA660165|AA660165 00002 MtrHE Medicago truncatula cDNA 5' si... 40 0.28  
 emb|Z34868|ATTS3597 A. thaliana transcribed sequence; clone FAF... 40 0.28  
 dbj|D39131|RICR2302A Rice cDNA, partial sequence (R2302\_1A). 40 0.28  
 gb|AA963968|AA963968 UI-R-C0-gs-b-05-0-UI.s1 UI-R-C0 Rattus nor... 40 0.28  
 gb|AA866346|AA866346 UI-R-A0-bm-a-05-0-UI.s1 UI-R-A0 Rattus nor... 40 0.28  
 gb|AI044437|AI044437 UI-R-C1-js-e-06-0-UI.s1 UI-R-C1 Rattus nor... 40 0.28  
 dbj|D41811|RICS4634A Rice cDNA, partial sequence (S4634\_1A). 40 0.28  
 dbj|C19261|C19261 Rice cDNA, partial sequence (E10176\_1A) 40 0.28  
 dbj|D48409|RICS14588A Rice cDNA, partial sequence (S14588\_1A). 40 0.28  
 dbj|C26556|C26556 Rice cDNA, partial sequence (C12586\_1A) 40 0.28  
 dbj|D47831|RICS13548A Rice cDNA, partial sequence (S13548\_1A). 40 0.28  
 dbj|C72152|C72152 Rice cDNA, partial sequence (E1094\_3A) 40 0.28  
 dbj|D46553|RICS11305A Rice cDNA, partial sequence (S11305\_2A). 40 0.28  
 gb|AI028926|AI0289 (and many others of similar score)

## SEQ ID NO:565

emb|X68308|OOLPLIP O.ovis mRNA for lipoprotein lipase 40 1.2  
 gb|AE000660|HUAEE000660 Homo sapiens T-cell receptor alpha delta... 40 1.2  
 emb|AL022333|HS474I12 Human DNA sequence \*\*\* SEQUENCING IN PROG... 38 4.6  
 emb|Z12618|CFTRG C.fasciculata gene encoding trypanothione redu... 38 4.6  
 gb|M81651|HUMSEMIIB Human semenogelin II (SEMGII) gene, complet... 38 4.6  
 gb|M96980|HUMMYT1A Homo sapiens myelin transcription factor 1 (... 38 4.6  
 gb|U89688|ACU89688 Acanthamoeba castellanii myosin-I binding pr... 38 4.6  
 gb|AC002497|AC002497 Human Cosmid g1940a142 from 7q31.3, comple... 38 4.6  
 gb|M81652|HUMSMNGLN Homo sapiens semenogelin II mRNA, complete ... 38 4.6  
 gb|M25665|HUMNCF1A Human neutrophil cytosol factor 1 (NCF-47k) ... 38 4.6  
 gb|M73325|TRFTRPREDC Crithidia fasciculata trypanothione reduct... 38 4.6  
 gb|M73324|TRFTRPREDB Crithidia fasciculata trypanothione reduct... 38 4.6  
 emb|X92589|MMSEMIIGN M.mulatta semenogelin II gene 38 4.6  
 emb|Z47556|HSSG1SG2 H.sapiens genes for semenogelin I and semen... 38 4.6  
 gb|AC004753|AC004753 Homo sapiens chromosome 16, cosmid clone R... 38 4.6  
 gb|M55067|HUMNADPHO Human 47-kD autosomal chronic granulomatous... 38 4.6

gb|M73323|TRFTRPREDA Crithidia fasciculata trypanothione reduct... 38 4.6

#### HUMAN ESTs

gb|R11942|R11942 yf54c05.r1 Homo sapiens cDNA clone 25950 5'. 656 0.0  
 gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130  
 gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94\_24 5' ... 133 5e-29  
 gb|R37032|R37032 yf54c05.s1 Homo sapiens cDNA clone 25950 3'. 44 0.036  
 gb|AA661650|AA661650 nv02h12.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA261982|AA261982 zs20d03.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA588219|AA588219 no24c11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA250891|AA250891 zs06c06.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA244177|AA244177 nc05a02.r1 NCI\_CGAP\_Pr1 Homo sapiens cDNA ... 38 2.2  
 gb|AA715147|AA715147 nv10d05.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA659887|AA659887 nv03a10.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA627890|AA627890 nq70a08.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA603596|AA603596 np27b11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA613738|AA613738 np25h09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA715248|AA715248 nv10h06.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AI038487|AI038487 ow25d12.x1 Soares parathyroid tumor NbHPA ... 38 2.2  
 gb|AA252786|AA252786 zs26f10.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA287819|AA287819 zs50h04.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA564176|AA564176 nj04c08.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA643870|AA643870 np26h07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA280371|AA280371 zt05f07.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|R00687|R00687 ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2  
 gb|AA587820|AA587820 nj06h05.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA588443|AA588443 no22c11.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA568385|AA568385 nl88f06.s1 NCI\_CGAP\_Co10 Homo sapiens cDNA... 38 2.2  
 gb|AA281831|AA281831 zt06c08.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2  
 gb|AA689530|AA689530 ns66e07.r1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA688300|AA688300 nv14a09.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA687962|AA687962 nv13h04.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA526586|AA526586 ni96f11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA642589|AA642589 nq73f04.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA541594|AA541594 ni89g07.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA... 38 2.2  
 gb|AA278713|AA278713 zs76h02.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2  
 gb|T58661|T58661 ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2  
 gb|AA689473|AA689473 ns66e07.s1 NCI\_CGAP\_Pr22 Homo sapiens cDNA... 38 2.2  
 gb|AA459023|AA459023 aa26a09.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA... 38 2.2

dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07  
gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2  
gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2  
gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2  
gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2  
gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2  
gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2  
gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8  
gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8  
gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 2.8  
gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8  
gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8  
gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8  
gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8  
dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044\_1A). 36 2.8  
gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8  
gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8  
dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786\_1A). 36 2.8  
gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8  
dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612\_1A). 36 2.8  
gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8  
dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620\_1A). 36 2.8  
gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8  
gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

We claim:



1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

2. The method of claim 1, wherein the agent is selected from the group consisting of

(a)

a nucleotide acid molecule comprising NA group 1 nucleic acid molecules

or a fragment thereof,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules or

a fragment thereof,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules

or a fragment thereof,

(d)

an antibody that binds to an expression product of NA group 1 nucleic

acids,

(e)

an antibody that binds to an expression product of NA group 3 nucleic

acids,

(f)  
an antibody that binds to an expression product of NA group 17 nucleic acids,

(g)  
and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

(h)  
an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and

(I)  
an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3. The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

4. The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5. A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

5

the protein,

(ii)

a peptide derived from the protein,

10

(iii)

an antibody which selectively binds the protein or peptide, and

(iv)

cytolytic T cells specific for a complex of the peptide derived from the

15

protein and an MHC molecule,

as a determination of regression, progression or onset of said condition.

6.

The method of claim 5, wherein the sample is a body fluid, a body

effusion or a tissue.

20

7.

The method of claim 5, wherein the step of monitoring comprises

contacting the sample with a detectable agent selected from the group consisting of

(a)

25

an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii), and

30

(c)

a cell which presents the complex of the peptide and MHC molecule of

(iv).

5

8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group

15 11 molecule.

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group 12 molecule.

20 13. The method of claim 5, wherein the nucleic acid molecule is a NA Group 13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group 14 molecule.

25

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group 15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group

30 16 molecule.

17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

5 18. A pharmaceutical preparation for a human subject comprising  
an agent which when administered to the subject enriches selectively the  
presence of complexes of an HLA molecule and a human cancer associated antigen, and  
a pharmaceutically acceptable carrier, wherein the human cancer  
associated antigen is a fragment of a human cancer associated antigen precursor encoded by a  
10 nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises  
a plurality of agents, each of which enriches selectively in the subject complexes of an HLA  
molecule and a different human cancer associated antigen.

15

20. The pharmaceutical preparation of claim 19, wherein the plurality is at  
least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid  
20 molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected  
from the group consisting of

(1) an isolated polypeptide comprising the human cancer associated  
25 antigen, or a functional variant thereof,

(2) an isolated nucleic acid operably linked to a promoter for expressing  
the isolated polypeptide, or functional variant thereof,

(3) a host cell expressing the isolated polypeptide, or functional variant  
thereof, and

(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an  
5 adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.

10 25. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.

15 26. The pharmaceutical preparation of claim 18, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof.

20 27. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

25 29. The pharmaceutical preparation of claim 25, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.

30 30. The pharmaceutical preparation of claim 25, wherein the cell is nonproliferative.

31. A composition comprising  
an isolated agent that binds selectively a PP Group 1 polypeptide.
32. The composition of matter of claim 31, wherein the agent binds selectively  
5 a PP Group 3 polypeptide.
33. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 11 polypeptide.
- 10 34. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 12 polypeptide.
35. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 13 polypeptide.
- 15 36. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 14 polypeptide.
37. The composition of matter of claim 31, wherein the agent binds selectively  
20 a PP Group 15 polypeptide.
38. The composition of matter of claim 31, wherein the agent binds selectively  
a PP Group 16 polypeptide.
- 25 39. The composition of claims 31-38, wherein the agent is a plurality of  
different agents that bind selectively at least two, at least three, at least four, or at least five  
different such polypeptides.
40. The composition of claims 31-38, wherein the agent is an antibody.

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising  
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic  
5 agent.

43. The composition of matter of claim 42, wherein the conjugate is of the  
agent and a therapeutic or diagnostic that is a toxin.

10 44. A pharmaceutical composition comprising an isolated nucleic acid  
molecule selected from the group consisting of:

(1)

NA Group 1 molecules, and

15

(2)

NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic  
acid molecule comprises a NA Group 3 or NA Group 4 molecule.

20

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic  
acid molecule comprises at least two isolated nucleic acid molecules coding for two different  
polypeptides, each polypeptide comprising a different human cancer associated antigen.

25

47. The pharmaceutical composition of claims 44-46 further comprising an  
expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host  
cell recombinantly expressing the isolated nucleic acid molecule.

30



49. A pharmaceutical composition comprising  
an isolated polypeptide comprising a PP Group 1 or a PP Group 2  
polypeptide, and  
a pharmaceutically acceptable carrier.

5

50. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

10 51. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptide comprises at least two different polypeptides, each comprising a different human  
cancer associated antigen.

52. The pharmaceutical composition of claim 49, wherein the isolated  
15 polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptides are PP  
Group 12 polypeptides or HLA binding fragments thereof.

20

54. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

55. The pharmaceutical composition of claim 49, wherein the isolated  
25 polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated  
polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

30

57. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 16 polypeptides or HLA binding fragments thereof.

58. The pharmaceutical composition of claims 49-57, further comprising an  
5 adjuvant.

59. An isolated nucleic acid molecule comprising a NA Group 3 molecule.

60. An isolated nucleic acid molecule comprising a NA Group 4 molecule.

10

61. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 11 molecule or a fragment thereof.

62. The isolated nucleic acid molecule of claims 59-60, wherein the molecule  
15 is a Group 12 molecule or a fragment thereof.

63. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 13 molecule or a fragment thereof.

20 64. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 14 molecule or a fragment thereof.

65. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 15 molecule or a fragment thereof.

25

66. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 16 molecule or a fragment thereof.

67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid  
consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of  
5 sufficient length to represent a sequence unique within the human genome, and identifying a  
nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

10

provided that the fragment includes a sequence of contiguous nucleotides  
which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1

(correct?),

15

(2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of  
contiguous nucleotides is selected from the group consisting of:

20

(1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

25

at least four contiguous nucleotides nonidentical to the sequence group,

(4)

at least five contiguous nucleotides nonidentical to the sequence group,

(5)

30

at least six contiguous nucleotides nonidentical to the sequence group,

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

70. The isolated nucleic acid molecule of claim 67, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

71. An expression vector comprising an isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

73. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims 71, 72, or 73.

75. A host cell transformed or transfected with an expression vector of claim 71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising  
a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

(a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

5 85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated  
10 antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)

a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

15

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

(c)

20

a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes  
25 of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(i)

removing an immunoreactive cell containing sample from the subject,

(ii)

contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

(iii)

introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

10 (I)  
identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule

15 (ii)  
transfecting a host cell with a nucleic acid selected from the group consisting of

20 (a) the nucleic acid molecule identified,

(b)  
a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen,

25 (c)  
deletions, substitutions or additions to (a) or (b), and

30



(d)

degenerates of (a), (b), or (c);

(iii)

5 culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv)

10 introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

15 94. The method of claim 93, further comprising:

(a)

identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule,

20 wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

25 95. The method of claim 93, wherein the immune response comprises a B-cell response or a T cell response.

30 96. The method of claim 95, wherein the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising  
10 administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising  
20 administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in  
25 the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that  
30 the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

- 5 the protein;
- (i) identifying cells from the subject which express abnormal amounts of
  - (ii) isolating a sample of the cells;
  - (iii) cultivating the cells, and
  - (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

10

106. The method of claim 105, wherein the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

15

107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by  
20 aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid  
30 molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising

a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

HY-10-12	KKEPPPPKVVHPLIGLACEYGGGSDYEEEEEEQTPPPQPTAQPOKKEEQTKKNEEDKLTWNKLACLLCRRQFPNKEVL	970
LOC15	PEIVRNQDEENPLKRGVLAAYSGSDNHEE.....ELVERLESEEEKLADWKKMACLLCRRQFPNKDAL	662
DXS8237E	DLPRLASDDKTSPPRGLVAAAYSGSDNHEE.....EQERGPPEREEKLTDWQKLACLLCRRQFPNKEAL	233
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*Figure 1*

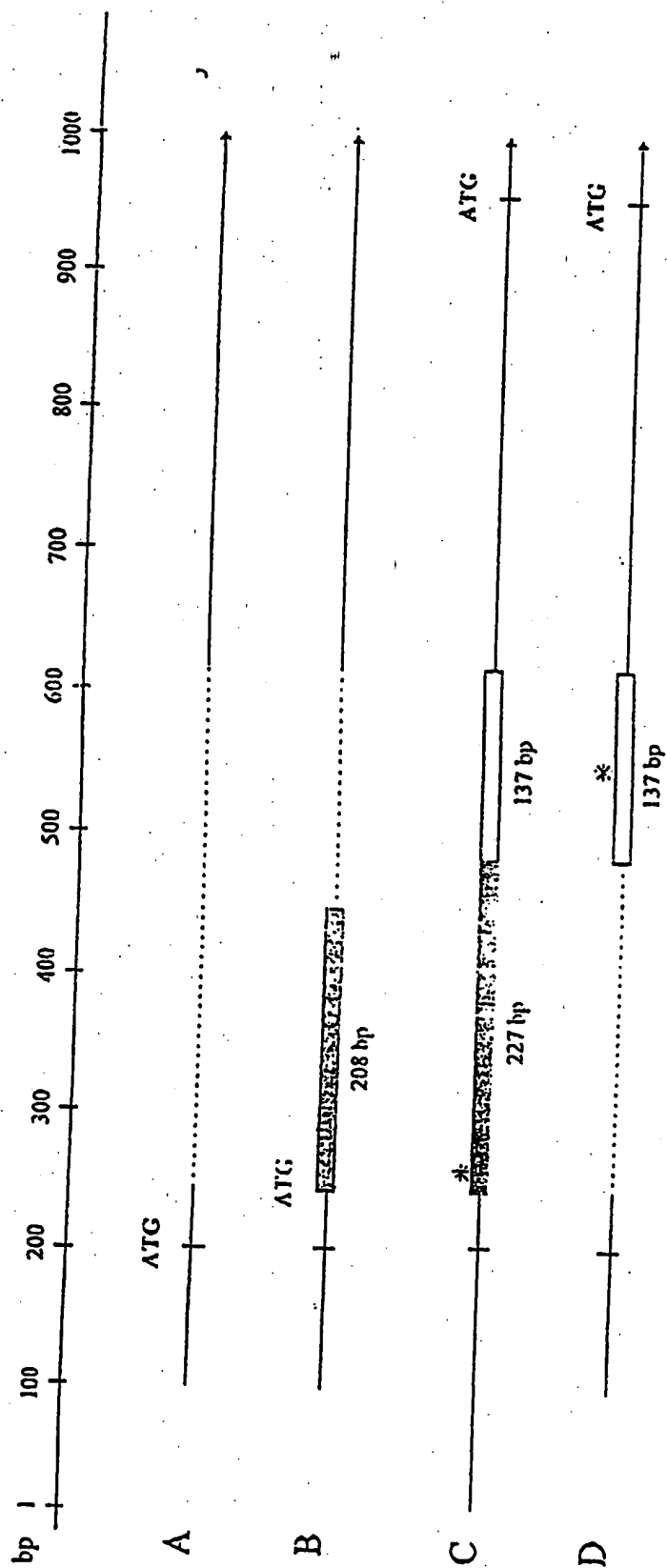




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Fig 2 (cont'd)





### Transcript Variant B

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Fig. 3a

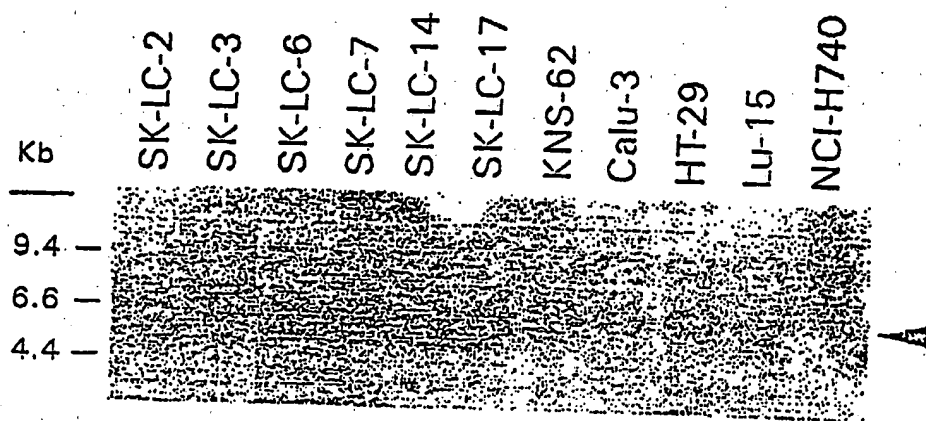
*Figure 3b.*

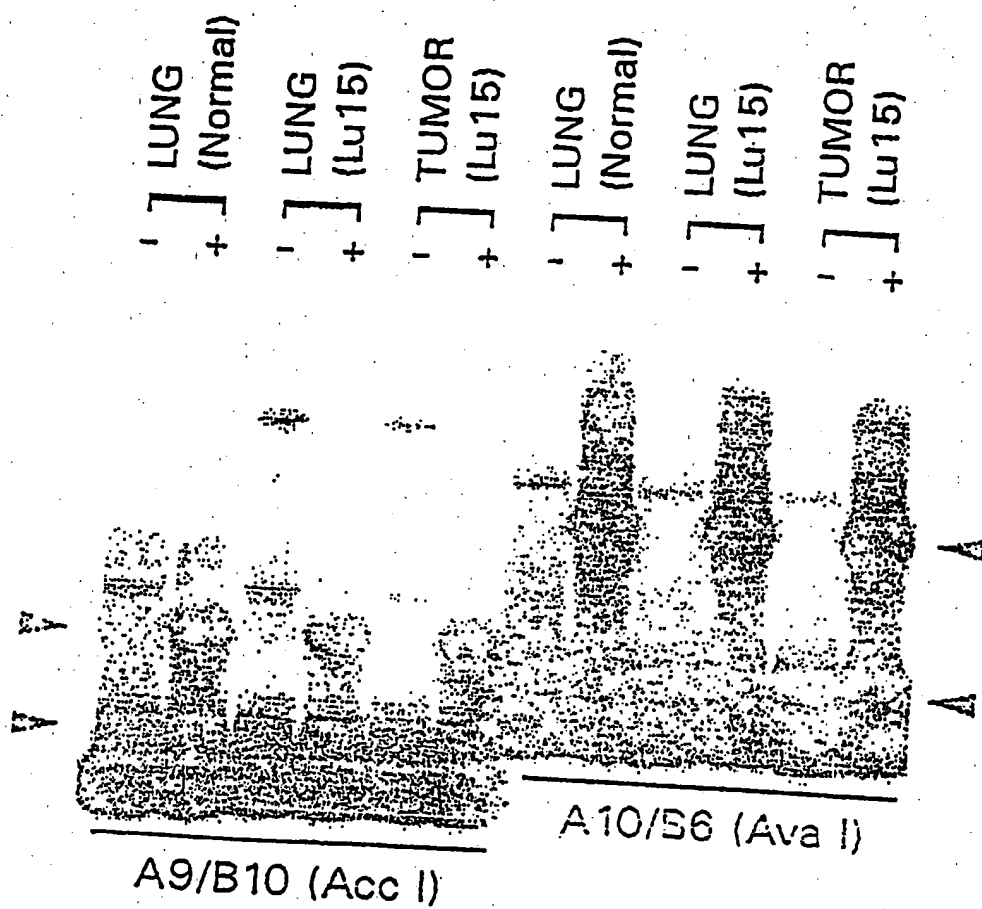
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*Figure 4*

*Figure 5*

## SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research  
Old, Lloyd J.  
Scanlan, Matthew J.  
Stockert, Elisabeth  
Gure, Ali  
Chen, Yao-Tseng  
Gout, Ivan  
O'Hare, Michael  
Obata, Yuichi  
Pfreundschuh, Michael  
Tureci, Ozlem  
Sahin, Ugur

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&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 24

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 25

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 26

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 28

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&lt;210&gt; 29

&lt;211&gt; 537

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 29

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&lt;210&gt; 30

&lt;211&gt; 3872

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 30

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&lt;210&gt; 31

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 31

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&lt;210&gt; 32

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 32

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&lt;210&gt; 33

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 33

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&lt;210&gt; 34

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 34

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&lt;210&gt; 35

&lt;211&gt; 679

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 35

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&lt;210&gt; 40

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 40

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&lt;210&gt; 41

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 41

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Pro Ser Val Arg Thr Gln Met Trp Leu Thr Glu Gln Leu Arg Thr Asn
 35          40          45
Pro Leu Glu Gly Arg Asn Thr Glu Asp Ser Tyr Ser Leu Ala Pro Trp
 50          55          60
Gln Gln Gln Gln Ile Glu Phe Arg Gln Gly Ser Glu Thr Pro Met Gln
 65          70          75          80
Val Leu Thr Gly Ser Ser Arg Gln Ser Tyr Ser Pro Gly Tyr Gln Asp
 85          90          95
Phe Ser Lys Trp Glu Ser Met Leu Lys Lys Glu Gly Leu Leu Arg Gln
100          105          110
Lys Glu Ile Val Asp Arg Gln Lys Gln Ile Thr His Leu Ile Arg Asp
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Asn Glu Leu Pro Ala His Ala Met Leu Gly His Tyr Val Asn Cys Glu
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<211> 95  
<212> PRT  
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Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu  
35 40 45  
Ile Phe Val Ser Phe Ala Phe Phe Arg Val Val Asn Ser Tyr Cys Pro  
50 55 60  
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<212> PRT  
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35 40 45  
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu  
50 55 60  
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly  
65 70 75 80  
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala  
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Glu Gly

<210> 44  
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<212> PRT  
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Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys  
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 Lys Thr His His Cys Ser Glu Glu Lys Glu Asp Glu Asp Tyr Met Pro  
 50 55 60  
 Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His  
 65 70 75 80  
 Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg  
 85 90 95  
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 Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys  
 35 40 45  
 Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg  
 50 55 60  
 Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser  
 65 70 75 80  
 Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly  
 85 90 95  
 Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val  
 100 105 110  
 Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met  
 115 120 125  
 Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser  
 130 135 140  
 Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp  
 145 150 155 160  
 Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser  
 165 170 175  
 Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala  
 180 185 190  
 Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser  
 195 200 205  
 Arg Leu Ala Thr Arg Ser  
 210

<210> 46  
 <211> 248  
 <212> PRT  
 <213> Homo Sapiens

&lt;400&gt; 46

Gly Ser Arg Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu  
 1 5 10 15  
 Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser  
 20 25 30  
 Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser  
 35 40 45  
 Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu  
 50 55 60  
 His Leu Leu Pro Gly Pro Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala  
 65 70 75 80  
 Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly  
 85 90 95  
 Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn  
 100 105 110  
 Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys  
 115 120 125  
 Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser  
 130 135 140  
 Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp  
 145 150 155 160  
 Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met  
 165 170 175  
 Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu  
 180 185 190  
 Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg  
 195 200 205  
 Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp  
 210 215 220  
 Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp  
 225 230 235 240  
 Glu Phe Ile His Lys Ile Thr Leu  
 245

&lt;210&gt; 47

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 47

Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu  
 1 5 10 15  
 Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile  
 20 25 30  
 Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val  
 35 40 45  
 Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr  
 50 55 60  
 Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys  
 65 70 75 80  
 Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser  
 85 90 95  
 Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His  
 100 105 110  
 Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly

115 120 125  
 Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile  
 130 135 140  
 Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys  
 145 150 155 160  
 Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys  
 165 170 175  
 Leu

<210> 48  
 <211> 102  
 <212> PRT  
 <213> Homo Sapiens

<400> 48  
 Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala  
 1 5 10 15  
 Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly  
 20 25 30  
 Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser  
 35 40 45  
 Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro  
 50 55 60  
 Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr  
 65 70 75 80  
 Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu  
 85 90 95  
 Pro Pro Leu Lys Asn Gly  
 100

<210> 49  
 <211> 179  
 <212> PRT  
 <213> Homo Sapiens

<400> 49  
 His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly  
 1 5 10 15  
 Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg  
 20 25 30  
 Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr  
 35 40 45  
 Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala  
 50 55 60  
 Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val  
 65 70 75 80  
 Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val  
 85 90 95  
 Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu  
 100 105 110  
 His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser  
 115 120 125  
 Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu  
 130 135 140



Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu  
 145 150 155 160  
 Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile  
 165 170 175  
 Cys Leu Leu

<210> 50  
 <211> 163  
 <212> PRT  
 <213> Homo Sapiens

<400> 50  
 Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys  
 1 5 10 15  
 Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu  
 20 25 30  
 Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile  
 35 40 45  
 Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly  
 50 55 60  
 His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly  
 65 70 75 80  
 Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln  
 85 90 95  
 Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln  
 100 105 110  
 Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala  
 115 120 125  
 Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg  
 130 135 140  
 Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu  
 145 150 155 160  
 Thr Leu Gln

<210> 51  
 <211> 164  
 <212> PRT  
 <213> Homo Sapiens

<400> 51  
 Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys  
 1 5 10 15  
 Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu  
 20 25 30  
 Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe  
 35 40 45  
 Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala  
 50 55 60  
 Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu  
 65 70 75 80  
 Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu  
 85 90 95  
 Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp

100 105 110  
 Glu Asp Glu Asp Phe Lys Arg Gln Asp Ala Met Lys Glu Ser Ile Pro  
 115 120 125  
 Phe Ala Val Val Gly Ser Cys Gln Val Val Arg Asp Gly Gly Asn Arg  
 130 135 140  
 Pro Val Arg Gly Arg Arg Tyr Ser Trp Gly Asn Val Glu Val Asn His  
 145 150 155 160  
 Ile Ala Ile Ser

<210> 52  
 <211> 600  
 <212> PRT  
 <213> Homo Sapiens

<400> 52  
 Met Cys Pro Arg Gln Val Asp Arg Ala Lys Glu Lys Gly Ile Gly Thr  
 1 5 10 15  
 Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala Glu Leu Glu Asn Ser  
 20 25 30  
 Ser Lys Glu Asn Glu Val Ile Glu Val Lys Ser Met Gly Glu Ser Gln  
 35 40 45  
 Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys Lys Tyr Cys Pro Tyr Ser  
 50 55 60  
 Thr Gln Asn Leu Asn Glu Phe Thr Glu His Val Asp Met Gln His Pro  
 65 70 75 80  
 Asn Val Ile Leu Asn Pro Leu Tyr Val Cys Ala Glu Cys Asn Phe Thr  
 85 90 95  
 Thr Lys Lys Tyr Asp Ser Leu Ser Asp His Asn Ser Lys Phe His Pro  
 100 105 110  
 Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile Lys Arg Asn Asn Gln Thr  
 115 120 125  
 Val Leu Glu Gln Ser Ile Glu Thr Thr Asn His Val Val Ser Ile Thr  
 130 135 140  
 Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp Ser Gly Ile Ser Val Ser  
 145 150 155 160  
 Lys Thr Pro Ile Met Lys Pro Gly Lys Pro Lys Ala Asp Ala Lys Lys  
 165 170 175  
 Val Pro Lys Lys Pro Glu Glu Ile Thr Pro Glu Asn His Val Glu Gly  
 180 185 190  
 Thr Ala Arg Leu Val Thr Asp Thr Ala Glu Ile Leu Ser Arg Leu Gly  
 195 200 205  
 Gly Val Glu Leu Leu Gln Asp Thr Leu Gly His Val Met Pro Ser Val  
 210 215 220  
 Gln Leu Pro Pro Asn Ile Asn Leu Val Pro Lys Val Pro Val Pro Leu  
 225 230 235 240  
 Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp Thr Asn Ala Thr Met Ile  
 245 250 255  
 Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr Gln Ala Glu Leu Ser Trp  
 260 265 270  
 Leu Thr Ala Ala Ser Lys His Pro Glu Glu His Ile Arg Ile Trp Phe  
 275 280 285  
 Ala Thr Gln Arg Leu Lys His Gly Ile Ser Trp Ser Pro Glu Glu Val  
 290 295 300  
 Glu Glu Ala Arg Lys Lys Met Phe Asn Gly Thr Ile Gln Ser Val Pro

305                      310                      315                      320  
 Pro Thr Ile Thr Val Leu Pro Ala Gln Leu Ala Pro Thr Lys Met Thr  
                                  325                      330                      335  
 Gln Pro Ile Leu Gln Thr Ala Leu Pro Cys Gln Ile Leu Gly Gln Thr  
                                  340                      345                      350  
 Ser Leu Val Leu Thr Gln Val Thr Ser Gly Ser Thr Thr Val Ser Cys  
                                  355                      360                      365  
 Ser Pro Ile Thr Leu Ala Val Ala Gly Val Thr Asn His Gly Gln Lys  
                                  370                      375                      380  
 Arg Pro Leu Val Thr Pro Gln Ala Ala Pro Glu Pro Lys Arg Pro His  
 385                                   390                      395                      400  
 Ile Ala Gln Val Pro Glu Pro Pro Pro Lys Val Ala Asn Pro Pro Leu  
                                  405                      410                      415  
 Thr Pro Ala Ser Asp Arg Lys Lys Thr Lys Glu Gln Ile Ala His Leu  
                                  420                      425                      430  
 Lys Ala Ser Phe Leu Gln Ser Gln Phe Pro Asp Asp Ala Glu Val Tyr  
                                  435                      440                      445  
 Arg Leu Ile Glu Val Thr Gly Leu Ala Arg Ser Glu Ile Lys Lys Trp  
                                  450                      455                      460  
 Phe Ser Asp His Arg Tyr Arg Cys Gln Arg Gly Ile Val His Ile Thr  
 465                                   470                      475                      480  
 Ser Glu Ser Leu Ala Lys Asp Gln Leu Ala Ile Ala Ala Ser Arg His  
                                  485                      490                      495  
 Gly Arg Thr Tyr His Ala Tyr Pro Asp Phe Ala Pro Gln Lys Phe Lys  
                                  500                      505                      510  
 Glu Lys Thr Gln Gly Gln Val Lys Ile Leu Glu Asp Ser Phe Leu Lys  
                                  515                      520                      525  
 Ser Ser Phe Pro Thr Gln Ala Glu Leu Asp Arg Leu Arg Val Glu Thr  
                                  530                      535                      540  
 Lys Leu Ser Arg Arg Glu Ile Asp Ser Trp Phe Ser Glu Arg Arg Lys  
 545                                   550                      555                      560  
 Leu Arg Asp Ser Met Glu Gln Ala Val Leu Asp Ser Met Gly Ser Gly  
                                  565                      570                      575  
 Gln Lys Arg Pro Arg Cys Gly Lys Pro Pro Met Val Leu Cys Leu Asp  
                                  580                      585                      590  
 Ser Asn Ser Ser Pro Val Pro Ser  
                                  595                      600

<210> 53  
 <211> 163  
 <212> PRT  
 <213> Homo Sapiens

<400> 53  
 Arg Lys Ser Trp Glu His Lys Glu Glu Ile Ser Glu Ala Glu Pro Gly  
 1                                   5                                   10                                   15  
 Gly Gly Ser Leu Gly Asp Gly Arg Pro Pro Glu Glu Ser Ala His Glu  
                                  20                                   25                                   30  
 Met Met Glu Glu Glu Glu Glu Ile Pro Lys Pro Lys Ser Val Val Ala  
                                  35                                   40                                   45  
 Pro Pro Gly Ala Pro Lys Lys Glu His Val Asn His Val Ala Gly Lys  
                                  50                                   55                                   60  
 Ser Thr Ile Gly Gly Gln Ile Met Tyr Leu Thr Gly Met Val Asp Lys  
 65                                   70                                   75                                   80  
 Arg Thr Leu Glu Lys Tyr Glu Arg Glu Ala Lys Glu Lys Asn Arg Glu

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<210> 54
<211> 155
<212> PRT
<213> Homo Sapiens
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<210> 55
<211> 112
<212> PRT
<213> Homo Sapiens
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Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr  
                     85                    90                    95  
 Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly  
                     100                    105                    110

<210> 56  
 <211> 151  
 <212> PRT  
 <213> Homo Sapiens

<400> 56  
 Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe  
   1                    5                    10                    15  
 Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu  
                     20                    25                    30  
 Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His  
                     35                    40                    45  
 Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala  
                     50                    55                    60  
 Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys  
   65                    70                    75                    80  
 Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu  
                     85                    90                    95  
 Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys  
                     100                    105                    110  
 Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr  
                     115                    120                    125  
 Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu  
                     130                    135                    140  
 Ala Gly Ser Asp Leu Arg Leu  
   145                    150

<210> 57  
 <211> 220  
 <212> PRT  
 <213> Homo Sapiens

<400> 57  
 Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His  
   1                    5                    10                    15  
 Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser  
                     20                    25                    30  
 Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys  
                     35                    40                    45  
 Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn  
                     50                    55                    60  
 Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp  
   65                    70                    75                    80  
 Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn  
                     85                    90                    95  
 Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser  
                     100                    105                    110  
 Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu  
                     115                    120                    125  
 Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

130                      135                      140  
 Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg  
 145                      150                      155                      160  
 Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr  
                     165                      170                      175  
 Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr  
                     180                      185                      190  
 Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu  
                     195                      200                      205  
 Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser  
                     210                      215                      220

<210> 58  
 <211> 101  
 <212> PRT  
 <213> Homo Sapiens

<400> 58  
 Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser  
 1                      5                      10                      15  
 Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn  
                     20                      25                      30  
 Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu Leu Gly Ser  
                     35                      40                      45  
 Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys  
                     50                      55                      60  
 Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr  
 65                      70                      75                      80  
 Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly  
                     85                      90                      95  
 Thr Arg Asn Leu Cys  
                     100

<210> 59  
 <211> 43  
 <212> PRT  
 <213> Homo Sapiens

<400> 59  
 Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn  
 1                      5                      10                      15  
 Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu  
                     20                      25                      30  
 Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu  
                     35                      40

<210> 60  
 <211> 210  
 <212> PRT  
 <213> Homo Sapiens

<400> 60  
 Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile  
 1                      5                      10                      15  
 Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

20 25 30  
 Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr Ala Asn  
 35 40 45  
 Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys Asn Leu  
 50 55 60  
 Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys Leu Glu  
 65 70 75 80  
 Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln Phe Lys  
 85 90 95  
 Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly Glu Leu  
 100 105 110  
 Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu Val Glu  
 115 120 125  
 Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln Asn Ile  
 130 135 140  
 Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala Ala Arg  
 145 150 155 160  
 Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser Asn Ser  
 165 170 175  
 Leu Pro Gly Leu Met Met Leu Arg Asn Lys Gly Val Ser Glu Lys Tyr  
 180 185 190  
 Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys Thr Ser Gln  
 195 200 205  
 Arg Lys  
 210

<210> 61  
 <211> 40  
 <212> PRT  
 <213> Homo Sapiens

<400> 61  
 Thr Pro Gly Pro Gly Ala Gly Phe Tyr Ala Cys Pro Ala Arg Pro Leu  
 1 5 10 15  
 Val Ser Gly Ile Tyr Ser Phe Arg Trp Val Arg Gly Leu Ala Asp Gln  
 20 25 30  
 Glu Arg Asn Trp Gly Leu Ser Gln  
 35 40

<210> 62  
 <211> 238  
 <212> PRT  
 <213> Homo Sapiens

<400> 62  
 His Glu Ala Arg Leu Lys Arg Ala Ser Ala Pro Thr Phe Asp Asn Asp  
 1 5 10 15  
 Tyr Ser Leu Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Val Ser Gln  
 20 25 30  
 Ala Val Glu Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys  
 35 40 45  
 Leu Pro Ser Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val  
 50 55 60  
 Asp Ser Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg  
 65 70 75 80

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys  
                     85                    90                    95  
 Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile  
                     100                    105                    110  
 Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu  
                     115                    120                    125  
 Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu  
                     130                    135                    140  
 Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr  
                     145                    150                    155                    160  
 Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu  
                     165                    170                    175  
 Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr  
                     180                    185                    190  
 Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu  
                     195                    200                    205  
 Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln  
                     210                    215                    220  
 Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu  
                     225                    230                    235

<210> 63  
 <211> 146  
 <212> PRT  
 <213> Homo Sapiens

<400> 63  
 Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe  
   1                    5                    10                    15  
 Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln  
                     20                    25                    30  
 Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg  
                     35                    40                    45  
 Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro  
                     50                    55                    60  
 Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu  
                     65                    70                    75                    80  
 Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu  
                     85                    90                    95  
 Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His  
                     100                    105                    110  
 Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp  
                     115                    120                    125  
 Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg  
                     130                    135                    140  
 Gly Lys  
 145

<210> 64  
 <211> 63  
 <212> PRT  
 <213> Homo Sapiens

<400> 64  
 Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe



1                      5                      10                      15  
 Ser Pro Asn Pro Arg Ile Val Ser Val Asn Ala Ser Tyr Ser Leu Ser  
                                  20                      25                      30  
 Asn Glu Ser Ser Leu Glu Gln Val Tyr Thr Leu Lys Met Ser Phe Ile  
                                  35                      40                      45  
 Ala Ser Asn Thr Tyr His Asn Gln Leu Tyr Lys Glu Gly Phe Leu  
                                  50                      55                      60

<210> 65  
 <211> 199  
 <212> PRT  
 <213> Homo Sapiens

<400> 65  
 Glu Ala Pro Asp Ser Ala Glu Gly Thr Thr Leu Thr Val Leu Pro Glu  
 1                      5                      10                      15  
 Gly Glu Glu Leu Pro Leu Cys Val Ser Glu Ser Asn Gly Leu Glu Leu  
                                  20                      25                      30  
 Pro Pro Ser Ala Ala Ser Asp Glu Pro Leu Gln Glu Pro Leu Glu Ala  
                                  35                      40                      45  
 Asp Arg Thr Ser Glu Glu Leu Thr Glu Ala Lys Thr Pro Thr Ser Ser  
                                  50                      55                      60  
 Pro Glu Lys Pro Gln Glu Leu Val Thr Ala Glu Val Ala Ala Pro Ser  
 65                      70                      75                      80  
 Thr Ser Ser Ser Ala Thr Ser Ser Pro Glu Gly Pro Ser Pro Ala Arg  
                                  85                      90                      95  
 Pro Pro Arg Arg Arg Thr Ser Ala Asp Val Glu Ile Arg Gly Gln Gly  
                                  100                      105                      110  
 Thr Gly Arg Pro Gly Gln Pro Pro Gly Pro Lys Val Leu Arg Lys Leu  
                                  115                      120                      125  
 Pro Gly Arg Leu Val Thr Val Val Glu Glu Lys Glu Leu Val Arg Arg  
                                  130                      135                      140  
 Arg Arg Gln Gln Arg Gly Ala Ala Ser Thr Leu Val Pro Gly Val Ser  
 145                      150                      155                      160  
 Glu Thr Ser Ala Ser Pro Gly Ser Pro Ser Val Arg Ser Met Ser Gly  
                                  165                      170                      175  
 Pro Glu Ser Ser Pro Pro Ile Gly Gly Pro Cys Glu Ala Ala Pro Ser  
                                  180                      185                      190  
 Ser Ser Leu Pro Thr Pro Pro  
 195

<210> 66  
 <211> 1599  
 <212> DNA  
 <213> Homo Sapiens

<400> 66  
 ttctttgaaa cattattatt cagaacgaag gagaatgata cagatacact ggctgaggtg 60  
 ttttgaggtg cattgaaatg ttccatgctg ttacttaggt taacatgttc ttgaggtacc 120  
 atgccatgga ttaaaaggaa atttggtgaag tggcttcac ctaaagcact tactagggaa 180  
 gctatgcgaa attattttaaa agggtaaggg gatcaaatag tacttatcct tcatgcaaaa 240  
 gttgtacaga agtcatatgg caatcaaaaa atttttttt gccctcccc ttgtgtatat 300  
 cttatgggca gtggatggaa gaaaaaaaaa gaacaaatga aatgcgatgg ttgttctgaa 360  
 cacagctctc atccatgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420  
 ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtacatatc tgattcagac 480

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aagcaaaagc acttcatttt ttctgtaaag gtgttctatg gcaacggtga tgacattggt 540
gtgttcctca gcaagtagat aaaagtcac tcacaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgtctcagga acaaagggtg ctctgttttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca 720
cagcagtggt gagcatttta cattcaattc ttggatgatg atggatcaga aggagaagaa 780
ttcacagtct gagatgccta cattcattat ggacaaacat gcaaacttgt gtgetcagtt 840
actggcatgg cactcccaag attgataatt atgaaagtgt ataagcatat cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat tttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
agagaaccaa ataaagagat gataaatgat ggcgcttctt ggacaatcat tagcacagat 1080
aaggcagggt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcaactccaa tttacgagtg tggtttgggg gggtagaagc tgaaactatg 1260
tacagggtgt gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaagggt 1320
tgagatggg tccggcaacc agtccaggtt ccagtaactt tgggtccgaaa tgatggaatc 1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccgcg gccacattgc 1440
agtgcagcag gagcaatcct tctagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaacgcc agcacaatt caaccagtgt cacatcatct 1560
acagccacag tggtatccta actaccgtct ttttgctag 1599

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&lt;210&gt; 67

&lt;211&gt; 729

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 67

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Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
1      5      10      15
Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
20     25     30
Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
35     40     45
Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
50     55     60
Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65     70     75     80
Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
85     90     95
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
100    105    110
Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
115    120    125
Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
130    135    140
Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
145    150    155    160
Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
165    170    175
Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
180    185    190
Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
195    200    205
Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
210    215    220
Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe

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225		230		235		240
His Val Lys Val Leu Asn Thr Ser Leu Lys Glu Lys Phe Asn Gly Lys						
	245		250		255	
Lys Ile Ile Ile Ile Ser Asp Tyr Leu Glu Tyr Asp Ser Leu Leu Glu						
	260		265		270	
Val Asn Glu Glu Ser Thr Val Ser Glu Ala Gly Pro Asn Gln Thr Phe						
	275		280		285	
Glu Val Pro Asn Lys Ile Ile Asn Arg Ala Lys Glu Thr Leu Lys Ile						
	290		295		300	
Asp Ile Leu His Lys Lys Gln Ala Ser Gly Asn Ile Val Tyr Gly Val Phe						
	305		310		315	
Met Leu His Lys Lys Thr Val Asn Gln Lys Thr Thr Ile Tyr Glu Ile						
	325		330		335	
Gln Asp Asp Arg Gly Lys Met Asp Val Val Gly Thr Gly Gln Cys His						
	340		345		350	
Asn Ile Pro Cys Glu Glu Gly Asp Lys Leu Gln Leu Phe Cys Phe Arg						
	355		360		365	
Leu Arg Lys Lys Asn Gln Met Ser Lys Leu Ile Ser Glu Met His Ser						
	370		375		380	
Phe Ile Gln Ile Lys Lys Lys Thr Asn Pro Arg Asn Asn Asp Pro Lys						
	385		390		395	
Ser Met Lys Leu Pro Gln Glu Gln Arg Gln Leu Pro Tyr Pro Ser Glu						
	405		410		415	
Ala Ser Thr Thr Phe Pro Glu Ser His Leu Arg Thr Pro Gln Met Pro						
	420		425		430	
Pro Thr Thr Pro Ser Ser Ser Phe Phe Thr Lys Lys Ser Glu Asp Thr						
	435		440		445	
Ile Ser Lys Met Asn Asp Phe Met Arg Met Gln Ile Leu Lys Glu Gly						
	450		455		460	
Ser His Phe Pro Gly Pro Phe Met Thr Ser Ile Gly Pro Ala Glu Ser						
	465		470		475	
His Pro His Thr Pro Gln Met Pro Pro Ser Thr Pro Ser Ser Ser Phe						
	485		490		495	
Leu Thr Thr Leu Lys Pro Arg Leu Lys Thr Glu Pro Glu Glu Val Ser						
	500		505		510	
Ile Glu Asp Ser Ala Gln Ser Asp Leu Lys Glu Val Met Val Leu Asn						
	515		520		525	
Ala Thr Glu Ser Phe Val Tyr Glu Pro Lys Glu Gln Lys Lys Met Phe						
	530		535		540	
His Ala Thr Val Ala Thr Glu Asn Glu Val Phe Arg Val Lys Val Phe						
	545		550		555	
Asn Ile Asp Leu Lys Glu Lys Phe Thr Pro Lys Lys Ile Ile Ala Ile						
	565		570		575	
Ala Asn Tyr Val Cys Arg Asn Gly Phe Leu Glu Val Tyr Pro Phe Thr						
	580		585		590	
Leu Val Ala Asp Val Asn Ala Asp Ala Asn Met Glu Ile Pro Lys Gly						
	595		600		605	
Leu Ile Arg Ser Ala Ser Val Thr Pro Lys Ile Asn Gln Leu Cys Ser						
	610		615		620	
Gln Thr Lys Gly Ser Phe Val Asn Gly Val Phe Glu Val His Lys Lys						
	625		630		635	
Asn Val Arg Gly Glu Phe Thr Tyr Tyr Glu Ile Gln Asp Asn Thr Gly						
	645		650		655	
Lys Met Glu Val Val Val His Gly Arg Leu Asn Thr Ile Asn Cys Glu						
	660		665		670	

Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser  
 675 680 685  
 Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val  
 690 695 700  
 Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser  
 705 710 715 720  
 Met Glu Thr Ser Pro Asp Phe Phe Phe  
 725

&lt;210&gt; 68

&lt;211&gt; 754

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 68

Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro  
 1 5 10 15  
 Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu  
 20 25 30  
 Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe  
 35 40 45  
 Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro  
 50 55 60  
 Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys  
 65 70 75 80  
 Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln  
 85 90 95  
 Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr  
 100 105 110  
 Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln  
 115 120 125  
 Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile  
 130 135 140  
 Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly  
 145 150 155 160  
 Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His  
 165 170 175  
 Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn  
 180 185 190  
 Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His  
 195 200 205  
 Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln  
 210 215 220  
 Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr  
 225 230 235 240  
 Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro  
 245 250 255  
 Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu  
 260 265 270  
 Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln  
 275 280 285  
 Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys  
 290 295 300  
 His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala  
 305 310 315 320

Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu  
 325 330 335  
 His Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val  
 340 345 350  
 Lys Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala  
 355 360 365  
 Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro  
 370 375 380  
 Asp His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu  
 385 390 395 400  
 Phe Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu  
 405 410 415  
 Pro Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu  
 420 425 430  
 Ser Ser Ser Glu Glu Ser Ser Ser Glu Ser Ser Ser Glu Glu Glu  
 435 440 445  
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Ser Glu Ser Ser Asp  
 450 455 460  
 Ser Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu  
 465 470 475 480  
 Arg Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser  
 485 490 495  
 Lys Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys  
 500 505 510  
 Ala Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly  
 515 520 525  
 Pro Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser  
 530 535 540  
 Gly Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro  
 545 550 555 560  
 Ser Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala  
 565 570 575  
 Pro Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser  
 580 585 590  
 Arg Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn  
 595 600 605  
 Lys Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala  
 610 615 620  
 Arg Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp  
 625 630 635 640  
 Phe Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val  
 645 650 655  
 Leu Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys  
 660 665 670  
 Pro Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu  
 675 680 685  
 Leu Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys  
 690 695 700  
 Lys Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln  
 705 710 715 720  
 Gln Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Ser Asp Ser  
 725 730 735  
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp  
 740 745 750  
 Ser Gly

<210> 69  
 <211> 210  
 <212> PRT  
 <213> Homo Sapiens

<400> 69  
 Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr  
 1 5 10 15  
 Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu  
 20 25 30  
 Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro  
 35 40 45  
 Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His  
 50 55 60  
 Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro  
 65 70 75 80  
 Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu  
 85 90 95  
 Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro  
 100 105 110  
 Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu  
 115 120 125  
 Gln Phe Leu Gln Gln Glu Leu Leu Ile Asn Ile Thr Glu His Glu Leu  
 130 135 140  
 Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu  
 145 150 155 160  
 Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly  
 165 170 175  
 Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys  
 180 185 190  
 Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu  
 195 200 205  
 Val Gln  
 210

<210> 70  
 <211> 621  
 <212> PRT  
 <213> Homo Sapiens

<400> 70  
 Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr  
 1 5 10 15  
 His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly  
 20 25 30  
 Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr  
 35 40 45  
 Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu  
 50 55 60  
 Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp  
 65 70 75 80  
 Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly  
 85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys  
 100 105 110  
 Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu  
 115 120 125  
 Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala  
 130 135 140  
 Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val  
 145 150 155 160  
 Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp  
 165 170 175  
 Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp  
 180 185 190  
 Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe  
 195 200 205  
 Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp  
 210 215 220  
 Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys  
 225 230 235 240  
 Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala  
 245 250 255  
 Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn  
 260 265 270  
 Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys  
 275 280 285  
 Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys  
 290 295 300  
 Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val  
 305 310 315 320  
 Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu  
 325 330 335  
 Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu  
 340 345 350  
 Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp  
 355 360 365  
 Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys  
 370 375 380  
 Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala  
 385 390 395 400  
 Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu  
 405 410 415  
 Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg  
 420 425 430  
 Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly  
 435 440 445  
 Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys  
 450 455 460  
 Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile  
 465 470 475 480  
 Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala  
 485 490 495  
 Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His  
 500 505 510  
 Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu  
 515 520 525  
 His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

530	535	540
Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys		
545	550	555
Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg		560
	565	570
Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys		575
	580	585
Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala		590
	595	600
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys		605
610	615	620

<210> 71  
 <211> 267  
 <212> PRT  
 <213> Homo Sapiens

<400> 71
Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp
1 5 10 15
Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn
20 25 30
Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro
35 40 45
Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu
50 55 60
Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp
65 70 75 80
Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe
85 90 95
Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn
100 105 110
Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu
115 120 125
Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys
130 135 140
Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile
145 150 155 160
Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala
165 170 175
Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile
180 185 190
Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys
195 200 205
Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu
210 215 220
Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln
225 230 235 240
Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys
245 250 255
Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr
260 265

<210> 72  
 <211> 1752



&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 72

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Arg Glu Lys Arg Arg Arg Lys Ser Val Glu Asp Arg Phe Asp Gln Gln
 1           5           10           15
Lys Asn Asp Tyr Asp Gln Leu Gln Lys Ala Arg Gln Cys Glu Lys Glu
 20           25           30
Asn Leu Gly Trp Gln Lys Leu Glu Ser Glu Lys Ala Ile Lys Glu Lys
 35           40           45
Glu Tyr Glu Ile Glu Arg Leu Arg Val Leu Leu Gln Glu Glu Gly Thr
 50           55           60
Arg Lys Arg Glu Tyr Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr
 65           70           75           80
Asn Glu Glu Met Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn
 85           90           95
Ile Thr Lys Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp
 100          105          110
Ser Lys Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg
 115          120          125
Asp Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
 130          135          140
Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys Ala
 145          150          155          160
Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile Glu Leu
 165          170          175
Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg His Lys Gln
 180          185          190
Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile
 195          200          205
Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala Lys Arg Arg Trp Glu
 210          215          220
Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn Asn Tyr Asp Glu Glu Ile
 225          230          235          240
Ile Ser Leu Lys Asn Gln Phe Glu Thr Glu Ile Asn Ile Thr Lys Thr
 245          250          255
Thr Ile His Gln Leu Thr Met Gln Lys Glu Glu Asp Thr Ser Gly Tyr
 260          265          270
Arg Ala Gln Ile Asp Asn Leu Thr Arg Glu Asn Arg Ser Leu Ser Glu
 275          280          285
Glu Ile Lys Arg Leu Lys Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu
 290          295          300
Arg Arg Val Glu Glu Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu
 305          310          315          320
Val Ser Gln Arg Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr
 325          330          335
Gln Met Arg Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp
 340          345          350
Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys
 355          360          365
Gln Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
 370          375          380
Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn Ser
 385          390          395          400
Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln Glu Leu

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Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys  
 850 855 860  
 Gln Leu Ile Asp Lys Thr Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys  
 865 870 875 880  
 Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala  
 885 890 895  
 Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu  
 900 905 910  
 Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met  
 915 920 925  
 Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg  
 930 935 940  
 Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp  
 945 950 955 960  
 Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly  
 965 970 975  
 Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile  
 980 985 990  
 Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala  
 995 1000 1005  
 Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu  
 1010 1015 1020  
 Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr  
 1025 1030 1035 104  
 Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro  
 1045 1050 1055  
 Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg  
 1060 1065 1070  
 Ile Glu Pro His Thr Gly Leu Leu Leu Ser Val Gln Lys Arg Ser  
 1075 1080 1085  
 Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val  
 1090 1095 1100  
 Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly  
 1105 1110 1115 112  
 Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln  
 1125 1130 1135  
 Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys  
 1140 1145 1150  
 Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr  
 1155 1160 1165  
 Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp  
 1170 1175 1180  
 Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly  
 1185 1190 1195 120  
 Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala  
 1205 1210 1215  
 Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe  
 1220 1225 1230  
 Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu  
 1235 1240 1245  
 Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser  
 1250 1255 1260  
 His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu  
 1265 1270 1275 128  
 Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

	1285		1290		1295
Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu					
	1300		1305		1310
Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys					
	1315		1320		1325
Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys					
	1330		1335		1340
Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val					
	1345		1350		1355
Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu					
	1365		1370		1375
Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser					
	1380		1385		1390
Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln					
	1395		1400		1405
Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe					
	1410		1415		1420
Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp					
	1425		1430		1435
Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser					
	1445		1450		1455
Gly Val Ser Asp Asp Val Phe Ser Ser Ser Arg His Glu Ser Val Ser					
	1460		1465		1470
Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser					
	1475		1480		1485
Ser Phe Ser Asp Thr Leu Glu Ser Ser Pro Ile Ala Ala Ile Phe					
	1490		1495		1500
Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg					
	1505		1510		1515
Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala					
	1525		1530		1535
Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu					
	1540		1545		1550
Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser					
	1555		1560		1565
Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly					
	1570		1575		1580
Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro					
	1585		1590		1595
Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly					
	1605		1610		1615
Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile					
	1620		1625		1630
Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr					
	1635		1640		1645
Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile					
	1650		1655		1660
Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly					
	1665		1670		1675
Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser					
	1685		1690		1695
Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser					
	1700		1705		1710
Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg					
	1715		1720		1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser  
 1730 1735 1740  
 Phe Ser Ser Ser Ser Ile Gly His  
 1745 1750

<210> 73  
 <211> 1978  
 <212> PRT  
 <213> Homo Sapiens

<400> 73  
 Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg  
 1 5 10 15  
 Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met  
 20 25 30  
 Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala  
 35 40 45  
 Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met  
 50 55 60  
 Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro  
 65 70 75 80  
 Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys  
 85 90 95  
 Gly Lys Pro His Gly Ser Arg Trp Asp Asp Glu Pro His Ile Ser Ala  
 100 105 110  
 Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser  
 115 120 125  
 Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu  
 130 135 140  
 Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr  
 145 150 155 160  
 Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp  
 165 170 175  
 Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln  
 180 185 190  
 Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val  
 195 200 205  
 Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu  
 210 215 220  
 Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn  
 225 230 235 240  
 Glu Phe Gln Ser Gln Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn  
 245 250 255  
 Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met  
 260 265 270  
 Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu  
 275 280 285  
 Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val  
 290 295 300  
 Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser  
 305 310 315 320  
 Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro  
 325 330 335  
 Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro  
 340 345 350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly  
 355 360 365  
 Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro  
 370 375 380  
 Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp  
 385 390 395 400  
 Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr  
 405 410 415  
 Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn  
 420 425 430  
 Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser  
 435 440 445  
 Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp  
 450 455 460  
 Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu  
 465 470 475 480  
 Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser  
 485 490 495  
 Arg Arg Ser Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met  
 500 505 510  
 His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg  
 515 520 525  
 Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg  
 530 535 540  
 Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser  
 545 550 555 560  
 Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys  
 565 570 575  
 Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn  
 580 585 590  
 Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln  
 595 600 605  
 Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser  
 610 615 620  
 Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys  
 625 630 635 640  
 Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser  
 645 650 655  
 Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu  
 660 665 670  
 His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys  
 675 680 685  
 Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn  
 690 695 700  
 Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu  
 705 710 715 720  
 Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro  
 725 730 735  
 Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys  
 740 745 750  
 Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys  
 755 760 765  
 Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val  
 770 775 780  
 Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

785		790		795		800
Cys Val Ala Lys Val Asn Lys Ser Thr Gly Lys Ser Ala Ser Ser Val						
805		810		815		
Lys Ser Val Val Thr Val Ala Val Lys Gly Asn Lys Ala Ser Ile Lys						
820		825		830		
Thr Ala Lys Ser Gly Gly Lys Lys Ser Leu Glu Ala Lys Lys Thr Gly						
835		840		845		
Asn Val Lys Asn Lys Asp Ser Asn Lys Pro Val Thr Ile Pro Glu Asn						
850		855		860		
Ser Glu Ile Lys Thr Ser Ile Glu Val Lys Ala Thr Glu Asn Cys Ala						
865		870		875		880
Lys Glu Ala Ile Ser Asp Ala Ala Leu Glu Ala Thr Glu Asn Glu Pro						
885		890		895		
Leu Asn Lys Glu Thr Glu Glu Met Cys Val Met Leu Val Ser Asn Leu						
900		905		910		
Pro Asn Lys Gly Tyr Ser Val Glu Glu Val Tyr Asp Leu Ala Lys Pro						
915		920		925		
Phe Gly Gly Leu Lys Asp Ile Leu Ile Leu Ser Ser His Lys Lys Ala						
930		935		940		
Tyr Ile Glu Ile Asn Arg Lys Ala Ala Glu Ser Met Val Lys Phe Tyr						
945		950		955		960
Thr Cys Phe Pro Val Leu Met Asp Gly Asn Gln Leu Ser Ile Ser Met						
965		970		975		
Ala Pro Glu Asn Met Asn Ile Lys Asp Glu Glu Ala Ile Phe Ile Thr						
980		985		990		
Leu Val Lys Glu Asn Asp Pro Glu Ala Asn Ile Asp Thr Ile Tyr Asp						
995		1000		1005		
Arg Phe Val His Leu Asp Asn Leu Pro Glu Asp Gly Leu Gln Cys Val						
1010		1015		1020		
Leu Cys Val Gly Leu Gln Phe Gly Lys Val Asp His His Val Phe Ile						
1025		1030		1035		104
Ser Asn Arg Asn Lys Ala Ile Leu Gln Leu Asp Ser Pro Glu Ser Ala						
1045		1050		1055		
Gln Ser Met Tyr Ser Phe Leu Lys Gln Asn Pro Gln Asn Ile Gly Asp						
1060		1065		1070		
His Met Leu Thr Cys Ser Leu Ser Pro Lys Ile Asp Leu Pro Glu Val						
1075		1080		1085		
Gln Ile Glu His Asp Pro Glu Leu Glu Lys Glu Ser Pro Gly Leu Lys						
1090		1095		1100		
Asn Ser Pro Ile Asp Glu Ser Glu Val Gln Thr Ala Thr Asp Ser Pro						
1105		1110		1115		112
Ser Val Lys Pro Asn Glu Leu Glu Glu Glu Ser Thr Pro Ser Ile Gln						
1125		1130		1135		
Thr Glu Thr Leu Val Gln Gln Glu Glu Pro Cys Glu Glu Glu Ala Glu						
1140		1145		1150		
Lys Ala Thr Cys Asp Ser Asp Phe Ala Val Glu Thr Leu Glu Leu Glu						
1155		1160		1165		
Thr Gln Gly Glu Glu Val Lys Glu Glu Ile Pro Leu Val Ala Ser Ala						
1170		1175		1180		
Ser Val Ser Ile Glu Gln Phe Thr Glu Asn Ala Glu Glu Cys Ala Leu						
1185		1190		1195		120
Asn Gln Gln Met Phe Asn Ser Asp Leu Glu Lys Lys Gly Ala Glu Ile						
1205		1210		1215		
Ile Asn Pro Lys Thr Ala Leu Leu Pro Ser Asp Ser Val Phe Ala Glu						
1220		1225		1230		

Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu  
 1235 1240 1245  
 Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu  
 1250 1255 1260  
 Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile  
 1265 1270 1275 128  
 Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp  
 1285 1290 1295  
 Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu  
 1300 1305 1310  
 Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr  
 1315 1320 1325  
 Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu  
 1330 1335 1340  
 Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys  
 1345 1350 1355 136  
 Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr  
 1365 1370 1375  
 Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro  
 1380 1385 1390  
 Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val  
 1395 1400 1405  
 Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp  
 1410 1415 1420  
 Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu  
 1425 1430 1435 144  
 Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe  
 1445 1450 1455  
 Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser  
 1460 1465 1470  
 Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys  
 1475 1480 1485  
 Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp  
 1490 1495 1500  
 Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser  
 1505 1510 1515 152  
 Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Glu Pro Leu Phe Pro Phe  
 1525 1530 1535  
 Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn  
 1540 1545 1550  
 Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr  
 1555 1560 1565  
 Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Gly  
 1570 1575 1580  
 Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr  
 1585 1590 1595 160  
 Leu Asp Glu Ile Gly Glu Glu Glu Asp Ala Ala Ala His Leu Ala Gln  
 1605 1610 1615  
 Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met  
 1620 1625 1630  
 Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu  
 1635 1640 1645  
 Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr  
 1650 1655 1660  
 Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu



1665                      1670                      1675                      168  
 Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu  
                                  1685                      1690                      1695  
 Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly  
                                  1700                      1705                      1710  
 Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu  
                                  1715                      1720                      1725  
 Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser  
                                  1730                      1735                      1740  
 Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp  
 1745                      1750                      1755                      176  
 Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr  
                                  1765                      1770                      1775  
 Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val  
                                  1780                      1785                      1790  
 Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn  
                                  1795                      1800                      1805  
 Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu  
                                  1810                      1815                      1820  
 Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys  
 1825                      1830                      1835                      184  
 Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val  
                                  1845                      1850                      1855  
 Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro  
                                  1860                      1865                      1870  
 Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser  
                                  1875                      1880                      1885  
 Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp  
                                  1890                      1895                      1900  
 Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp  
 1905                      1910                      1915                      192  
 Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe  
                                  1925                      1930                      1935  
 Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His  
                                  1940                      1945                      1950  
 Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu  
                                  1955                      1960                      1965  
 Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg  
                                  1970                      1975

&lt;210&gt; 74

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 74

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala  
 1                      5                      10                      15  
 Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe  
                                  20                      25                      30  
 Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala  
                                  35                      40                      45  
 Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala  
 50                      55                      60  
 Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly

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65          70          75          80
Pro Glu Tyr Trp Asp Arg Glu Thr Gln Lys Tyr Lys Arg Gln Ala Gln
      85          90          95
Thr Asp Arg Val Ser Leu Arg Asn Leu Arg Gly Tyr Tyr Asn Gln Ser
      100          105          110
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly Cys Asp Val Gly
      115          120          125
Pro Asp Gly Arg Leu Leu Arg Gly Tyr Asp Gln Tyr Ala Tyr Asp Gly
      130          135          140
Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
145          150          155          160
Asp Thr Ala Ala Gln Ile Thr Gln Arg Lys Trp Glu Ala Ala Arg Glu
      165          170          175
Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Leu Cys Val Glu Trp Leu
      180          185          190
Arg Arg Tyr Leu Lys Asn Gly Lys Glu Thr Leu Gln Arg Ala Glu His
      195          200          205
Pro Lys Thr His Val Thr His His Pro Val Ser Asp His Glu Ala Thr
      210          215          220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225          230          235          240
Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
      245          250          255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
      260          265          270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
      275          280          285
Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
      290          295          300
Thr Ile Pro Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val
305          310          315          320
Leu Ala Val Leu Gly Ala Val Val Ala Val Val Met Cys Arg Arg Lys
      325          330          335
Ser Ser Gly Gly Lys Gly Gly Ser Cys Ser Gln Ala Ala Ser Ser Asn
      340          345          350
Ser Ala Gln Gly Ser Asp Glu Ser Leu Ile Ala Cys Lys Ala
      355          360          365

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<210> 75
<211> 240
<212> PRT
<213> Homo Sapiens

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<400> 75
Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
1      5      10      15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
      20      25      30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
      35      40      45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
      50      55      60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65      70      75      80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp

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<210> 76
<211> 953
<212> PRT
<213> Homo Sapiens
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-47-

225		230		235		240									
Asn	Leu	Leu	Met	Ala	Tyr	Gln	Ile	Cys	Phe	Asp	Leu	Tyr	Glu	Ser	Ala
				245					250						255
Ser	Gln	Gln	Phe	Leu	Ser	Ser	Val	Ile	Gln	Asn	Leu	Arg	Thr	Val	Gly
			260					265						270	
Thr	Pro	Ile	Ala	Ser	Val	Pro	Gly	Ser	Thr	Asn	Thr	Gly	Thr	Val	Pro
		275					280					285			
Gly	Ser	Glu	Lys	Asp	Ser	Asp	Ser	Met	Glu	Thr	Glu	Glu	Lys	Thr	Ser
	290					295					300				
Ser	Ala	Phe	Val	Gly	Lys	Thr	Pro	Glu	Ala	Ser	Pro	Glu	Pro	Lys	Asp
305					310					315					320
Gln	Thr	Leu	Lys	Met	Ile	Lys	Ile	Leu	Ser	Gly	Glu	Met	Ala	Ile	Glu
			325						330					335	
Leu	His	Leu	Gln	Phe	Leu	Ile	Arg	Asn	Asn	Asn	Thr	Asp	Leu	Met	Ile
		340					345						350		
Leu	Lys	Asn	Thr	Lys	Asp	Ala	Val	Arg	Asn	Ser	Val	Cys	His	Thr	Ala
	355						360					365			
Thr	Val	Ile	Ala	Asn	Ser	Phe	Met	His	Cys	Gly	Thr	Thr	Ser	Asp	Gln
	370					375					380				
Phe	Leu	Arg	Asp	Asn	Leu	Glu	Trp	Leu	Ala	Arg	Ala	Thr	Asn	Trp	Ala
385				390					395						400
Lys	Phe	Thr	Ala	Thr	Ala	Ser	Leu	Gly	Val	Ile	His	Lys	Gly	His	Glu
			405					410					415		
Lys	Glu	Ala	Leu	Gln	Leu	Met	Ala	Thr	Tyr	Leu	Pro	Lys	Asp	Thr	Ser
	420						425					430			
Pro	Gly	Ser	Ala	Tyr	Gln	Glu	Gly	Gly	Gly	Leu	Tyr	Ala	Leu	Gly	Leu
	435					440						445			
Ile	His	Ala	Asn	His	Gly	Gly	Asp	Ile	Ile	Asp	Tyr	Leu	Leu	Asn	Gln
	450				455				460						
Leu	Lys	Asn	Ala	Ser	Asn	Asp	Ile	Val	Arg	His	Gly	Gly	Ser	Leu	Gly
465				470					475						480
Leu	Gly	Leu	Ala	Ala	Met	Gly	Thr	Ala	Arg	Gln	Asp	Val	Tyr	Asp	Leu
			485					490					495		
Leu	Lys	Thr	Asn	Leu	Tyr	Gln	Asp	Asp	Ala	Val	Thr	Gly	Glu	Ala	Ala
		500					505					510			
Gly	Leu	Ala	Leu	Gly	Leu	Val	Met	Leu	Gly	Ser	Lys	Asn	Ala	Gln	Ala
	515					520						525			
Ile	Glu	Asp	Met	Val	Gly	Tyr	Ala	Gln	Glu	Thr	Gln	His	Glu	Lys	Ile
	530				535						540				
Leu	Arg	Gly	Leu	Ala	Val	Gly	Ile	Ala	Leu	Val	Met	Tyr	Gly	Arg	Met
545				550					555						560
Glu	Glu	Ala	Asp	Ala	Leu	Ile	Glu	Ser	Leu	Cys	Arg	Asp	Lys	Asp	Pro
			565					570					575		
Ile	Leu	Arg	Arg	Ser	Gly	Met	Tyr	Thr	Val	Ala	Met	Ala	Tyr	Cys	Gly
		580					585					590			
Ser	Gly	Asn	Asn	Lys	Ala	Ile	Arg	Arg	Leu	Leu	His	Val	Ala	Val	Ser
	595						600					605			
Asp	Val	Asn	Asp	Asp	Val	Arg	Ser	Ala	Ala	Val	Glu	Ser	Leu	Gly	Phe
	610					615					620				
Ile	Leu	Phe	Arg	Thr	Pro	Glu	Gln	Cys	Pro	Ser	Val	Val	Ser	Leu	Leu
625				630					635						640
Ser	Glu	Ser	Tyr	Asn	Pro	His	Val	Arg	Tyr	Gly	Ala	Ala	Met	Ala	Leu
			645					650					655		
Gly	Ile	Cys	Cys	Ala	Gly	Thr	Gly	Asn	Lys	Glu	Ala	Ile	Asn	Leu	Leu
		660					665					670			

Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu  
 675 680 685  
 Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro  
 690 695 700  
 Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys  
 705 710 715 720  
 His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile  
 725 730 735  
 Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr  
 740 745 750  
 Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln  
 755 760 765  
 Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr  
 770 775 780  
 Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val  
 785 790 795 800  
 Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro  
 805 810 815  
 Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val  
 820 825 830  
 Leu Ser Ile Thr Ala Lys Ala Lys Lys Lys Glu Lys Glu Lys Glu Lys  
 835 840 845  
 Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu  
 850 855 860  
 Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn  
 865 870 875 880  
 Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu  
 885 890 895  
 Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile  
 900 905 910  
 Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val  
 915 920 925  
 Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro  
 930 935 940  
 Pro Glu Pro Phe Glu Tyr Ile Asp Asp  
 945 950

&lt;210&gt; 77

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 77

Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg  
 1 5 10 15  
 Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala  
 20 25 30  
 Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln  
 35 40 45  
 Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn  
 50 55 60  
 Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg  
 65 70 75 80  
 Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val  
 85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu  
 100 105 110  
 Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala  
 115 120 125  
 Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu  
 130 135 140  
 Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu  
 145 150 155 160  
 Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr  
 165 170 175  
 Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser  
 180 185 190  
 Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro  
 195 200 205  
 Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu  
 210 215 220  
 Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val  
 225 230 235 240  
 Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp  
 245 250 255  
 Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly  
 260 265 270  
 Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser  
 275 280 285  
 Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn  
 290 295 300  
 Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr  
 305 310 315 320  
 Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu  
 325 330 335

<210> 78  
 <211> 117  
 <212> PRT  
 <213> Homo Sapiens

<400> 78  
 Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala  
 1 5 10 15  
 Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr  
 20 25 30  
 Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val  
 35 40 45  
 Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu  
 50 55 60  
 Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly  
 65 70 75 80  
 Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu  
 85 90 95  
 Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln  
 100 105 110  
 Ser Gln Lys Ala Lys  
 115

<210> 79

<211> 614  
 <212> PRT  
 <213> Homo Sapiens

<400> 79  
 Arg Ser Gly Gln Pro Arg Ala Glu Gly Leu Gly Ala Gly Ala Ala Gly  
 1 5 10 15  
 Pro Leu Arg Ala Met Ala Ala Pro Val Lys Gly Asn Arg Lys Gln Ser  
 20 25 30  
 Thr Glu Gly Asp Ala Leu Asp Pro Pro Ala Ser Pro Lys Pro Ala Gly  
 35 40 45  
 Lys Gln Asn Gly Ile Gln Asn Pro Ile Ser Leu Glu Asp Ser Pro Glu  
 50 55 60  
 Ala Gly Gly Glu Arg Glu Glu Glu Gln Glu Arg Glu Glu Gln Ala  
 65 70 75 80  
 Phe Leu Val Ser Leu Tyr Lys Phe Met Lys Glu Arg His Thr Pro Ile  
 85 90 95  
 Glu Arg Val Pro His Leu Gly Phe Lys Gln Ile Asn Leu Trp Lys Ile  
 100 105 110  
 Tyr Lys Ala Val Glu Lys Leu Gly Ala Tyr Glu Leu Val Thr Gly Arg  
 115 120 125  
 Arg Leu Trp Lys Asn Val Tyr Asp Glu Leu Gly Gly Ser Pro Gly Ser  
 130 135 140  
 Thr Ser Ala Ala Thr Cys Thr Arg Arg His Tyr Glu Arg Leu Val Leu  
 145 150 155 160  
 Pro Tyr Val Arg His Leu Lys Gly Glu Asp Asp Lys Pro Leu Pro Thr  
 165 170 175  
 Ser Lys Pro Arg Lys Gln Tyr Lys Met Ala Lys Glu Asn Arg Gly Asp  
 180 185 190  
 Asp Gly Ala Thr Glu Arg Pro Lys Lys Ala Lys Glu Glu Arg Arg Met  
 195 200 205  
 Asp Gln Met Met Pro Gly Lys Thr Lys Ala Asp Ala Ala Asp Pro Ala  
 210 215 220  
 Pro Leu Pro Ser Gln Glu Pro Pro Arg Asn Ser Thr Glu Gln Gln Gly  
 225 230 235 240  
 Leu Ala Ser Gly Ser Ser Val Ser Phe Val Gly Ala Ser Gly Cys Pro  
 245 250 255  
 Glu Ala Tyr Lys Arg Leu Leu Ser Ser Phe Tyr Cys Lys Gly Thr His  
 260 265 270  
 Gly Ile Met Ser Pro Leu Ala Lys Lys Lys Leu Leu Ala Gln Val Ser  
 275 280 285  
 Lys Val Glu Ala Leu Gln Cys Gln Glu Glu Gly Cys Arg His Gly Ala  
 290 295 300  
 Glu Pro Gln Ala Ser Pro Ala Val His Leu Pro Glu Ser Pro Gln Ser  
 305 310 315 320  
 Pro Lys Gly Leu Thr Glu Asn Ser Arg His Arg Leu Thr Pro Gln Glu  
 325 330 335  
 Gly Leu Gln Ala Pro Gly Gly Ser Leu Arg Glu Glu Ala Gln Ala Gly  
 340 345 350  
 Pro Cys Pro Ala Ala Pro Ile Phe Lys Gly Cys Phe Tyr Thr His Pro  
 355 360 365  
 Thr Glu Val Leu Lys Pro Val Ser Gln His Pro Arg Asp Phe Phe Ser  
 370 375 380  
 Arg Leu Lys Asp Gly Val Leu Leu Gly Pro Pro Gly Lys Glu Gly Leu  
 385 390 395 400

Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro  
 405 410 415  
 Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys  
 420 425 430  
 Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser  
 435 440 445  
 Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys  
 450 455 460  
 Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg  
 465 470 475 480  
 Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala  
 485 490 495  
 Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu  
 500 505 510  
 Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro  
 515 520 525  
 Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu  
 530 535 540  
 Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala  
 545 550 555 560  
 Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro  
 565 570 575  
 Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser  
 580 585 590  
 Ala Trp His Ala Pro Pro Val Thr Thr Tyr Ala Ala Pro His Phe Phe  
 595 600 605  
 His Leu Asn Thr Lys Leu  
 610

<210> 80  
 <211> 114  
 <212> PRT  
 <213> Homo Sapiens

<400> 80  
 Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu  
 1 5 10 15  
 His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile  
 20 25 30  
 Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala  
 35 40 45  
 Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly  
 50 55 60  
 Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro  
 65 70 75 80  
 Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala  
 85 90 95  
 Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu  
 100 105 110  
 Phe Asp

<210> 81  
 <211> 596  
 <212> PRT



## &lt;213&gt; Homo Sapiens

&lt;400&gt; 81

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Met Arg Arg Ala His Glu Gly Arg Glu Ile Pro Ser Leu Gly Gly Ala
 1           5           10           15
Arg Arg Arg Glu Val Leu Gln Ala Gly Arg Ser Gln Arg Ala Ala Gly
 20           25           30
Arg Arg Arg Arg Arg Gln Glu Leu Glu Leu Gly Val Gly Ser Gly Arg
 35           40           45
Pro Gly Gly Pro Pro Pro Gly Pro Gly Arg Arg Gly Thr Cys Ala Ala
 50           55           60
Ala Leu Pro Pro Glu Trp Pro Arg Arg Arg Thr Gly Leu Pro Arg Arg
 65           70           75           80
Gly Pro Arg Pro Pro Leu Ala Met Ala Lys Trp Leu Asn Lys Tyr Phe
 85           90           95
Ser Leu Gly Asn Ser Lys Thr Lys Ser Pro Pro Gln Pro Pro Arg Pro
 100          105          110
Asp Tyr Arg Glu Gln Arg Arg Arg Gly Glu Arg Pro Ser Gln Pro Pro
 115          120          125
Gln Ala Val Pro Gln Ala Ser Ser Ala Ala Ser Ala Ser Cys Gly Pro
 130          135          140
Ala Thr Ala Ser Cys Phe Ser Ala Ser Ser Gly Ser Leu Pro Asp Asp
 145          150          155          160
Ser Gly Ser Thr Ser Asp Leu Ile Arg Ala Tyr Arg Ala Gln Lys Glu
 165          170          175
Arg His Phe Gln Asp Pro Tyr Asn Gly Pro Gly Ser Ser Leu Arg Lys
 180          185          190
Leu Arg Ala Met Cys Arg Leu Asp Tyr Cys Gly Gly Ser Gly Glu Pro
 195          200          205
Gly Gly Val Gln Arg Ala Phe Ser Ala Ser Ser Ala Ser Gly Ala Ala
 210          215          220
Gly Cys Cys Cys Ala Ser Ser Gly Ala Gly Ala Ala Ala Ser Ser Ser
 225          230          235          240
Ser Ser Ser Gly Ser Pro His Leu Tyr Arg Ser Ser Ser Glu Arg Arg
 245          250          255
Pro Ala Thr Pro Ala Glu Val Arg Tyr Ile Ser Pro Lys His Arg Leu
 260          265          270
Ile Lys Val Glu Ser Ala Ala Gly Gly Gly Ala Gly Asp Pro Leu Gly
 275          280          285
Gly Ala Cys Ala Gly Gly Arg Thr Trp Ser Pro Thr Ala Cys Gly Gly
 290          295          300
Lys Lys Leu Leu Asn Lys Cys Ala Ala Ser Ala Ala Glu Glu Ser Gly
 305          310          315          320
Ala Gly Lys Lys Asp Lys Val Thr Ile Ala Asp Asp Tyr Ser Asp Pro
 325          330          335
Phe Asp Ala Lys Asn Asp Leu Lys Ser Lys Ala Gly Lys Gly Glu Ser
 340          345          350
Ala Gly Tyr Met Glu Pro Tyr Glu Ala Gln Arg Ile Met Thr Glu Phe
 355          360          365
Gln Arg Gln Glu Ser Val Arg Ser Gln His Lys Gly Ile Gln Leu Tyr
 370          375          380
Asp Thr Pro Tyr Glu Pro Glu Gly Gln Ser Val Asp Ser Asp Ser Glu
 385          390          395          400
Ser Thr Val Ser Pro Arg Leu Arg Glu Ser Lys Leu Pro Gln Asp Asp
 405          410          415

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Asp Arg Pro Ala Asp Glu Tyr Asp Gln Pro Trp Glu Trp Asn Arg Val  
                   420                  425                  430  
 Thr Ser Pro Ala Leu Ala Ala Gln Phe Asn Gly Asn Glu Lys Arg Gln  
                   435                  440                  445  
 Ser Ser Pro Ser Pro Ser Arg Asp Arg Arg Arg Gln Leu Arg Ala Pro  
                   450                  455                  460  
 Gly Gly Gly Phe Lys Pro Ile Lys His Gly Ser Pro Glu Phe Cys Gly  
 465                  470                  475                  480  
 Ile Leu Gly Glu Arg Val Asp Pro Ala Val Pro Leu Glu Lys Gln Ile  
                   485                  490                  495  
 Trp Tyr His Gly Ala Ile Ser Arg Gly Asp Ala Glu Asn Leu Leu Arg  
                   500                  505                  510  
 Leu Cys Lys Glu Cys Ser Tyr Leu Val Arg Asn Ser Gln Thr Ser Lys  
                   515                  520                  525  
 His Asp Tyr Pro Leu Ser Leu Arg Ser Asn Gln Gly Phe Met His Met  
                   530                  535                  540  
 Lys Leu Ala Lys Thr Lys Glu Lys Tyr Val Leu Gly Gln Asn Ser Pro  
 545                  550                  555                  560  
 Pro Phe Asp Ser Val Pro Glu Val Ile His Tyr Tyr Thr Thr Arg Lys  
                   565                  570                  575  
 Leu Pro Ile Lys Gly Ala Glu His Leu Ser Leu Leu Tyr Pro Val Ala  
                   580                  585                  590  
 Val Arg Thr Leu  
                   595

<210> 82  
 <211> 207  
 <212> PRT  
 <213> Homo Sapiens

<400> 82  
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
 1                  5                  10                  15  
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
                   20                  25                  30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
                   35                  40                  45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
                   50                  55                  60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65                  70                  75                  80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
                   85                  90                  95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
                   100                  105                  110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
                   115                  120                  125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg  
                   130                  135                  140  
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro  
 145                  150                  155                  160  
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala  
                   165                  170                  175  
 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala  
                   180                  185                  190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
 195 200 205

<210> 83  
 <211> 429  
 <212> PRT  
 <213> Homo Sapiens

<400> 83

Glu Cys Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp  
 1 5 10 15  
 Cys Glu Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser  
 20 25 30  
 Ser Glu Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val  
 35 40 45  
 Ile Asn Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser  
 50 55 60  
 Glu Thr Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr  
 65 70 75 80  
 Phe Glu Ala Ile Gln Leu Asp Asp Glu His Ile Asp Ser Leu Ser Ser  
 85 90 95  
 Phe Lys Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp  
 100 105 110  
 Thr Pro Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser  
 115 120 125  
 Arg Arg Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg  
 130 135 140  
 His Asp Pro Arg Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg  
 145 150 155 160  
 Asp Val Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys  
 165 170 175  
 His Glu Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln  
 180 185 190  
 Val Arg Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile  
 195 200 205  
 Asp Asp Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro  
 210 215 220  
 Asp Leu Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg  
 225 230 235 240  
 Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu  
 245 250 255  
 Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg  
 260 265 270  
 Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala  
 275 280 285  
 Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu  
 290 295 300  
 Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr  
 305 310 315 320  
 Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn  
 325 330 335  
 Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu  
 340 345 350  
 Ser Phe Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His  
 355 360 365

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu  
 370 375 380  
 Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu  
 385 390 395 400  
 Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala  
 405 410 415  
 Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys  
 420 425

<210> 84  
 <211> 113  
 <212> PRT  
 <213> Homo Sapiens

<400> 84  
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr  
 1 5 10 15  
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu  
 20 25 30  
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val  
 35 40 45  
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val  
 50 55 60  
 Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln  
 65 70 75 80  
 Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp  
 85 90 95  
 Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val  
 100 105 110  
 Gly

<210> 85  
 <211> 258  
 <212> PRT  
 <213> Homo Sapiens

<400> 85  
 Met Ile Asn Ile Glu Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly  
 1 5 10 15  
 Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu  
 20 25 30  
 Ala His Ser Gln Ile Glu Lys Arg Arg Asp Lys Met Asn Ser Phe  
 35 40 45  
 Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg  
 50 55 60  
 Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys  
 65 70 75 80  
 Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro  
 85 90 95  
 Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala  
 100 105 110  
 Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe  
 115 120 125  
 Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130 135 140  
 Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys  
 145 150 155 160  
 Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu  
 165 170 175  
 Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly  
 180 185 190  
 Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met  
 195 200 205  
 Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser  
 210 215 220  
 Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His  
 225 230 235 240  
 Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile  
 245 250 255  
 Val Leu

<210> 86  
 <211> 569  
 <212> PRT  
 <213> Homo Sapiens

<400> 86  
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
 1 5 10 15  
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
 20 25 30  
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr  
 35 40 45  
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys  
 50 55 60  
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser  
 65 70 75 80  
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu  
 85 90 95  
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu  
 100 105 110  
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln  
 115 120 125  
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu  
 130 135 140  
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser  
 145 150 155 160  
 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe  
 165 170 175  
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser  
 180 185 190  
 Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg  
 195 200 205  
 Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg  
 210 215 220  
 Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu  
 225 230 235 240  
 Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile

245 250 255  
 Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn  
 260 265 270  
 Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp  
 275 280 285  
 His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly  
 290 295 300  
 Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu  
 305 310 315 320  
 Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys  
 325 330 335  
 Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu  
 340 345 350  
 Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys  
 355 360 365  
 Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala  
 370 375 380  
 Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr  
 385 390 395 400  
 Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp  
 405 410 415  
 Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys  
 420 425 430  
 Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp  
 435 440 445  
 Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys  
 450 455 460  
 Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu  
 465 470 475 480  
 Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn  
 485 490 495  
 Val His Lys Gln Arg Val Ala Glu Val Leu Asn Asp Pro Glu Asn Met  
 500 505 510  
 Glu Lys Arg Arg Ser Arg Glu Ser Leu Asn Val Asp Val Val Lys Tyr  
 515 520 525  
 Glu Ser Gly Pro Asp Gly Gly Glu Glu Val Ser Met Ser Val Glu Trp  
 530 535 540  
 Asn Gly Gly Val Ser Gly Arg Ala Ser Phe Cys Gly Lys Arg Gln Gln  
 545 550 555 560  
 Gln Gln Trp Pro Gly Arg Arg His Arg  
 565

&lt;210&gt; 87

&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 87

Met Glu Ala Leu Ile Pro Val Ile Asn Lys Leu Gln Asp Val Phe Asn  
 1 5 10 15  
 Thr Val Gly Ala Asp Ile Ile Gln Leu Pro Gln Ile Val Val Val Gly  
 20 25 30  
 Thr Gln Ser Ser Gly Lys Ser Ser Val Leu Glu Ser Leu Val Gly Arg  
 35 40 45  
 Asp Leu Leu Pro Arg Gly Thr Gly Ile Val Thr Arg Arg Pro Leu Ile

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Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile  
 500 505 510  
 Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val  
 515 520 525  
 Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser  
 530 535 540  
 Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile  
 545 550 555 560  
 Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly  
 565 570 575  
 Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met  
 580 585 590  
 Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys  
 595 600 605  
 Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn  
 610 615 620  
 Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu  
 625 630 635 640  
 Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu  
 645 650 655  
 Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His  
 660 665 670  
 Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly  
 675 680 685  
 Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu  
 690 695 700  
 Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu  
 705 710 715 720  
 Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp  
 725 730 735

&lt;210&gt; 88

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 88

Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly  
 1 5 10 15  
 Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val  
 20 25 30  
 Lys Leu Leu Leu Gln  
 35

&lt;210&gt; 89

&lt;211&gt; 1381

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 89

ccgcagccct agagccgccc aagggatggc gatggcgctac ttggcttgga gactggcgcg 60  
 gegtctgtgt ccgagttctc tgcaggtcnc tantttcccg gtagttcanc tgcncatgaa 120  
 tanaacagca atgagagccn ctncnaaaga ctttgaaaat tcaactgaatc nagtgaaact 180  
 ctngaaaaag gatccangaa acgaaatgaa nctnaaactc tncgcgctat atnancangc 240  
 cncgtgaanga cttgtntcat gccnaacca nggtgtnttg atttgatcna caaggggccca 300



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atgggaçaca tgggaatgcc ttggcancct gccnaagaa ctgccaggca naactatgtg 360
gatttggtgt ccantttgan tccntccttg gaatcctcna atcnngtgga ncctggaaca 420
nacaggaaat ccaactgggtt tgaaactctg gtggtgacct ccgaagatgg catcacaag 480
atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt 540
atgctgtcac ttaaagctgc cagcaaggat gactcaatca tcaactgttt aacaggaaat 600
ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc ccctggtgga 660
gtagaggaga aagctaaaaa taatgccgtt ttactgaggg aatttggtgg ctgttttata 720
gattttccta agcctctgat tgcagtggtc aatggtccag ctgtgggcat ctccgtcacc 780
ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt 840
agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc 900
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt 960
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc 1020
aggctgaagg catttgcaaa gcttccccc aatgccttga gaatttcaa agaggtaac 1080
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtcctcag 1140
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttata cagaaaatca 1200
aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct 1260
ctgatttcca gtactggaac taaataagct tcattgtgcc tttttagtg ctagaatata 1320
aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa 1380
a 1381

```

<210> 90  
 <211> 298  
 <212> PRT  
 <213> Homo Sapiens

<400> 90

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Thr Cys Met Pro Val Phe Asp Leu Ile Lys Gly Pro Met Gly His
1      5      10      15
Met Glu Cys Pro Trp Pro Ala Arg Thr Ala Arg Asn Tyr Val Asp Leu
20     25     30
Val Ser Leu Pro Ser Leu Glu Ser Ser Asn Val Pro Gly Thr Arg Lys
35     40     45
Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
50     55     60
Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
65     70     75     80
Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
85     90     95
Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
100    105    110
Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
115    120    125
Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
130    135    140
Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
145    150    155    160
Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
165    170    175
Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
180    185    190
Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
195    200    205
Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
210    215    220
Cys Ala Gln Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys

```

```
<210> 91
<211> 1514
<212> DNA
<213> Homo Sapiens
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```
<210> 92
<211> 407
<212> PRT
<213> Homo Sapiens
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Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile  
 50 55 60  
 Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp  
 65 70 75 80  
 Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu  
 85 90 95  
 Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly  
 100 105 110  
 Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly  
 115 120 125  
 Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr  
 130 135 140  
 Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu  
 145 150 155 160  
 Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu  
 165 170 175  
 Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu  
 180 185 190  
 Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly  
 195 200 205  
 Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn  
 210 215 220  
 Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala  
 225 230 235 240  
 Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys  
 245 250 255  
 Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Ile Lys His Asn  
 260 265 270  
 Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro  
 275 280 285  
 Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro  
 290 295 300  
 Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala  
 305 310 315 320  
 Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Gln Pro  
 325 330 335  
 Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val  
 340 345 350  
 Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly  
 355 360 365  
 Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu  
 370 375 380  
 Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro  
 385 390 395 400  
 Lys Asp Phe Asp Trp Glu Ile  
 405

&lt;210&gt; 93

&lt;211&gt; 2236

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 93

cctggcccggtcgcggtcgcggctctttccagctcctggcagccgggcacccgaaggaac  
 gggtcgtgcaacgacgcagctggacacatggccagccatggaccgaaaagtggcccgagaa

60

120

ttccggcata	aggtggattt	tctgattgaa	aatgatgcag	agaaggacta	tctctatgat	180
gtgctgcgaa	tgtaccacca	gaccatggac	gtggccgtgc	tcgtgggaga	cctgaagctg	240
gtcatcaatg	aaccagccg	tctgcctctg	tttgatgcc	ttcggccgct	gatcccactg	300
aagcaccagg	tggaatatga	tcagctgacc	ccccggcgct	ccaggaagct	gaaggagggtg	360
cgtctggacc	gtctgcaccc	cgaaggcctc	ggcctgagtg	tgcgtggtgg	cctggagttt	420
ggctgtgggc	tcttcatctc	ccacctcatc	aaaggcggtc	aggcagacag	cgctgggctc	480
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gaggtcatca	acctcattcg	aaccaagaaa	actgtgtcca	tcaaagtgag	acacatcggc	600
ctgatccccg	tgaaaagctc	tctgatgag	ccccctactt	ggcagtatgt	ggatcagttt	660
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gagaagaagg	tcttcatcag	cctggtaggc	tcccgaggcc	ttggctgcag	catttccagc	780
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atggggaagg	atgtccggct	cctacgcctc	aagaaggagg	gatccttaga	cctggccctg	1500
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ctccggcccc	acctcgtgaa	cacaaagcct	cggaccagcc	ttgagagagg	ccacatgaca	1860
cacaccagat	ggcatccttg	ggacctgaat	ctatcaccca	ggaatctcaa	actccctttg	1920
gccctgaacc	agggccagat	aaggaacagc	tcgggccact	tttttgaagg	ccaatgtgga	1980
ggaaagggag	cagccagccg	tttgggagaa	gatctcaagg	atccagactc	tcattccttt	2040
cctctggccc	agtgaatttg	gtctctccca	gctttggggg	actccttctc	tgaaccctaa	2100
taagacccca	ctggagtctc	tctctctcca	tccctctcct	ctgccctctg	ctctaattgc	2160
tgccaggatt	gtcactccaa	accttactct	gagctcatta	ataaaataaa	cagattttatt	2220
ttccagctta	aaaaaa					2236

&lt;210&gt; 94

&lt;211&gt; 652

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 94

Met	Asp	Arg	Lys	Val	Ala	Arg	Glu	Phe	Arg	His	Lys	Val	Asp	Phe	Leu
1				5					10					15	
Ile	Glu	Asn	Asp	Ala	Glu	Lys	Asp	Tyr	Leu	Tyr	Asp	Val	Leu	Arg	Met
			20					25					30		
Tyr	His	Gln	Thr	Met	Asp	Val	Ala	Val	Leu	Val	Gly	Asp	Leu	Lys	Leu
			35				40					45			
Val	Ile	Asn	Glu	Pro	Ser	Arg	Leu	Pro	Leu	Phe	Asp	Ala	Ile	Arg	Pro
			50				55				60				
Leu	Ile	Pro	Leu	Lys	His	Gln	Val	Glu	Tyr	Asp	Gln	Leu	Thr	Pro	Arg
65					70				75					80	
Arg	Ser	Arg	Lys	Leu	Lys	Glu	Val	Arg	Leu	Asp	Arg	Leu	His	Pro	Glu
				85				90					95		

Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu  
 100 105 110  
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu  
 115 120 125  
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser  
 130 135 140  
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val  
 145 150 155 160  
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro  
 165 170 175  
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser  
 180 185 190  
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys  
 195 200 205  
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys  
 210 215 220  
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His  
 225 230 235 240  
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp  
 245 250 255  
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys  
 260 265 270  
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile  
 275 280 285  
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu  
 290 295 300  
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln  
 305 310 315 320  
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Glu  
 325 330 335  
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu  
 340 345 350  
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu  
 355 360 365  
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu  
 370 375 380  
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg  
 385 390 395 400  
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp  
 405 410 415  
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys  
 420 425 430  
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile  
 435 440 445  
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu  
 450 455 460  
 Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val  
 465 470 475 480  
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile  
 485 490 495  
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp  
 500 505 510  
 Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln  
 515 520 525  
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

530                      535                      540  
 Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln  
 545                      550                      555                      560  
 Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr  
                          565                      570                      575  
 Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp  
                          580                      585                      590  
 His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu  
                          595                      600                      605  
 Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu  
                          610                      615                      620  
 Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu  
 625                      630                      635                      640  
 Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln  
                          645                      650

<210> 95  
 <211> 831  
 <212> DNA  
 <213> Homo Sapiens

<400> 95  
 cataactggg actcgcgcg ctcgaggtcg acactagtgg gatccaaaga attcggcacg 60  
 agaaaccaca atgccagat ctcaagtaga tgaagagttt ttgaagcaaa gtttaaagga 120  
 aaaacnattg cagaaaacat ttagattnta tgaaatatat aatnanancc aaanccatt 180  
 tgaanttaat nganccttac ctgtcntcac taaatcaggg ttntctgcg caccnaaggg 240  
 cngcccancg cctgctgtgt tggcttanta ggcctnagca tangggcagn tgcaatcctt 300  
 tcctectnng gcggcanatg ggcttctgga anaacccttn ccttatcccc ancgcaaggc 360  
 ggccccctccc ctgcccctnaa aggaaacctc ntggacncag ggaatatang gccaccttga 420  
 aggggtggact ggctatcntg gaagatcaga taccaccaag caatttggag acagttcctg 480  
 ttgagaataa ccacggtttc catgaaaaga cagcagcgct gaagcttgag gccgagggcg 540  
 aggccatgga agatgcagcc gcgccagggg acgaccgagg cggcacacag gagccagccc 600  
 cagtgcctgc tgagccggtt gacaacacta cctacaagaa cctgcagcat catgactaca 660  
 gcacgtacac cttcttagac ctcaacctcg aactctcaaa attcaggatg cctcagccct 720  
 cctcaggccg ggagtcacct cgacactgag ggccctcggg gtgaagatga accttcacc 780  
 gtcttcactg catcctggag tgcaaaaata aaatccactc aagagtcaaa a 831

<210> 96  
 <211> 184  
 <212> PRT  
 <213> Homo Sapiens

<400> 96  
 Arg Lys Asn Cys Arg Lys His Leu Asp Met Lys Tyr Ile Lys His Leu  
 1                      5                      10                      15  
 Leu Pro Tyr Leu Ser Ser Leu Asn Gln Gly Leu Arg His Arg Ala Ala  
                          20                      25                      30  
 Arg Leu Leu Cys Trp Leu Arg Pro His Gly Cys Asn Pro Phe Leu Leu  
                          35                      40                      45  
 Arg Met Gly Phe Trp Asn Pro Leu Ile Pro Ala Arg Arg Pro Leu Pro  
 50                      55                      60  
 Cys Pro Arg Lys Pro Gly Arg Glu Tyr Ala Thr Leu Lys Gly Gly Leu  
 65                      70                      75                      80  
 Ala Ile Glu Asp Gln Ile Pro Pro Ser Asn Leu Glu Thr Val Pro Val  
                          85                      90                      95

Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu  
 100 105 110  
 Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg  
 115 120 125  
 Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn  
 130 135 140  
 Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe  
 145 150 155 160  
 Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser  
 165 170 175  
 Ser Gly Arg Glu Ser Pro Arg His  
 180

<210> 97  
 <211> 1008  
 <212> DNA  
 <213> Homo Sapiens

<400> 97  
 gcaaggtctc caagtcccag ctcaaggtcc tttcccataa cctgtgcacg gtgctgaagg 60  
 ttcctcatga ccagattgcc cttgaagagc acttcaggga tgatgatgag ggtccagtgt 120  
 ccaaccaggg ctacatgcct tatttaaaca ggttcatttt ggaaaaggtc caagacaact 180  
 ttgacaagat tgaattcaat aggatgtgtt ggaccctctg tgtcaaaaaa aacctcacia 240  
 agaatcccct gctcattaca gaagaanatg catttaaaat atgggttatt ttcaactttt 300  
 tatctgagga caagtatcca ttaattattg tgcagaana gattgaatac ctgcttaaga 360  
 agcttacaga agctatggga ggaggttggc agcaagaaca atttgaacat tataaaatca 420  
 actttgatga cagtaaaaat ggcctttctg catgggaact tattgagctt attggaaatg 480  
 gacagtttag caaaggcatg gaccggcaga ctgtgtctat ggcaattaat gaagtcttta 540  
 atgaacttat attagatgtg ttaaagcagg gttacatgat gaaaaagggc cacagacgga 600  
 aaaactggac tgaacgatgg tttgtactaa aaccaacat aatttcttac tatgtgagtg 660  
 aggatctgaa ggataagaaa ggagacattc tcttgatga aaattgctgt gtagagtcct 720  
 tgcctgacaa agatggaaaag aaatgccttt ttctcgtaaa atgttttgat aagacttttg 780  
 aaatcagtg ttcagataag aanaanaaac aggagtggat tcaagccatt cattctacta 840  
 ttcattctgt gaagctgnac agccctccac canacaaaga agccnnccag cttctnaaan 900  
 aactccgnga gaatcatctg gctgaacaag angaactgga gcgacaaatg aangaactcc 960  
 aagcccgcga atgaaagcaa ncagcaagag ctggaaggcc ttncggaa 1008

<210> 98  
 <211> 312  
 <212> PRT  
 <213> Homo Sapiens

<400> 98  
 Lys Val Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Cys Thr  
 1 5 10 15  
 Val Leu Lys Val Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg  
 20 25 30  
 Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu  
 35 40 45  
 Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu  
 50 55 60  
 Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys  
 65 70 75 80  
 Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe  
 85 90 95

Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile  
 100 105 110  
 Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln  
 115 120 125  
 Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn  
 130 135 140  
 Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe  
 145 150 155 160  
 Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val  
 165 170 175  
 Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys  
 180 185 190  
 Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys  
 195 200 205  
 Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys  
 210 215 220  
 Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp  
 225 230 235 240  
 Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr  
 245 250 255  
 Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile  
 260 265 270  
 His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala  
 275 280 285  
 Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg  
 290 295 300  
 Gln Met Glu Leu Gln Ala Arg Gln  
 305 310

&lt;210&gt; 99

&lt;211&gt; 1009

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 99

ggctaagtga acataactcta ccacttggtc tgaagcccag cagtatctga tggataatcc 60  
 aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taatttgctt 120  
 tgaagaacac attcgggctt tagaaaagga ggaagaagaa gaaaaacaga agagtttgct 180  
 gagagaaagg agacgacagc gaaaaaatag ggaatcttct cagatatttt tagatgaatt 240  
 acatgaacat ggacaactgc attctatgtc atcttggatg gaattgtatc caactattag 300  
 ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt 360  
 caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaga 420  
 cattctaaag gataaaggat ttgtagttag agtaaacact acttttgaag attttgtggc 480  
 gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcttt 540  
 caatagttta ctagaaaagg cagaagcccg tgaacgtgaa agagaaaaag aagaggctcg 600  
 gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctctccgat 660  
 agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga 720  
 ggacataact ctagaatctg aaagaaaacg aatattttaa gattttatgc atgtgcttga 780  
 gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca 840  
 tcataggaaa cgttcccgct ctcgatcggg gtcagattca ngatgatgat gatagccatt 900  
 caaagaaaaa aagacagcga tgagaagtct cggctctgntt canaacattc ttccantngc 960  
 agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagt 1009

&lt;210&gt; 100

&lt;211&gt; 292



&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 100

Ala Asn Val Thr Tyr Ser Thr Thr Trp Ser Glu Ala Gln Gln Tyr Leu  
 1 5 10 15  
 Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp  
 20 25 30  
 Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu  
 35 40 45  
 Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg  
 50 55 60  
 Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu  
 65 70 75 80  
 His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr  
 85 90 95  
 Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro  
 100 105 110  
 Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys  
 115 120 125  
 Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp  
 130 135 140  
 Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala  
 145 150 155 160  
 Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile  
 165 170 175  
 Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg  
 180 185 190  
 Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala  
 195 200 205  
 Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala  
 210 215 220  
 Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu  
 225 230 235 240  
 Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met  
 245 250 255  
 His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys  
 260 265 270  
 His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg  
 275 280 285  
 Ser Gly Ser Asp  
 290

&lt;210&gt; 101

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 101

aggtgacaat agatatagaa gtacgttgat gtgcgaagat gtattttggt ttagccagcg 60  
 aggaaaaaag aatcagtttg attatacatt taccaaacat taagaattta atatggtaac 120  
 ttttatttca gtattaaaat agcaatttta tttattactt ttttatatat agaatttgac 180  
 accaaatttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240  
 acctggtgca ggaagcttca tctgaagatg tcttgggcgt tcatatggtg gacaaagaca 300  
 cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

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gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc 420
gtgacgaagg ctcttggggc aagccattgt gtccaccoga gatactctcg gagacgttgc 480
caggctctgt gaagaaaagg gtatgctttc catcagaaga tcatctagag gagtttatag 540
cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag 600
gcacccaaac caacggtgac ctggaagacc tggaggagca tgggccaggg cagacagtct 660
ctgaggaagc cacagaagtt cacatgatgg agggggaccc agacacactg gccgaacttc 720
tgatcagggg tgacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg 780
aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg 840
tgncagggga gnnnttctct gaggaagcca caggggttca catgatgcag gtggaccagg 900
ccacgctggc aaagagtgc ctggaagacc tggaggagca tgtgccagag cagacagtct 960
ctgaggaagc cacagggggtt cac 983

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&lt;210&gt; 102

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 102

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Met Val Asp Lys Asp Thr Glu Arg Asp Ile Glu Met Lys Arg Gln Leu
 1             5             10             15
Arg Arg Leu Arg Glu Leu His Leu Tyr Ser Thr Trp Lys Lys Tyr Gln
      20             25             30
Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
      35             40             45
Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
      50             55             60
Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
65             70             75             80
Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
      85             90             95
Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
      100            105            110
Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
      115            120            125
Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
      130            135            140
Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
145            150            155            160
Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
      165            170            175
Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
      180            185            190
Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
      195            200            205
Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
210            215            220
Glu Ala Thr Gly Val His
225            230

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&lt;210&gt; 103

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 103

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aatncccgct gcaggtcgac actagtggat ccaaagaatt cggcacgagg caagttctgg      60
gagctggaca cggaccacga cctgctcatc gacgcggacg acctggcgcg gcacaatgac      120
cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga      180
aaagtgcaga aggaagggaa gatcagctat gccgactttg tctgggtttt gatctctgag      240
gaagacaaaa aaacaccgac cagcatcgag tactggttcc gctgcatgga cctggacggg      300
gacggcgccc tgtccatgtt cgagctcgag tacttctacg aggagcagtg ccgaaggetg      360
gacagcatgg ccacgagggc cctgcccttc caggactgcc tctgccagat gctggacctg      420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc      480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcaaaagag      540
cagatctccc tgctcaggga cggtgacagc ggcggggccc agctctcgga ctgggagaag      600
tnccggccga agagtncgac atcctggtgg ccgangaaac cgtgggggana nccctgggga      660
agacgggttc naaggcgaac tcaccccent ggancanaaa ctgantgctg tgcgtcccc      720
gctgggcan aggccttctt ccaagcgctt cccgctgggg cgccgtggaa ctgttncaaa      780
ttccctgcg gggacaagaa cttgaaaccg ctgtganncc ccccnana accnccccg      840
gnt                                                                    843

```

<210> 104  
 <211> 197  
 <212> PRT  
 <213> Homo Sapiens

<400> 104

Arg	Cys	Arg	Ser	Thr	Leu	Val	Asp	Pro	Lys	Asn	Ser	Ala	Arg	Gly	Lys
1				5					10					15	
Phe	Trp	Glu	Leu	Asp	Thr	Asp	His	Asp	Leu	Leu	Ile	Asp	Ala	Asp	Asp
			20					25					30		
Leu	Ala	Arg	His	Asn	Asp	His	Ala	Leu	Ser	Thr	Lys	Met	Ile	Asp	Arg
			35				40					45			
Ile	Phe	Ser	Gly	Ala	Val	Thr	Arg	Gly	Arg	Lys	Val	Gln	Lys	Glu	Gly
			50				55				60				
Lys	Ile	Ser	Tyr	Ala	Asp	Phe	Val	Trp	Phe	Leu	Ile	Ser	Glu	Glu	Asp
					70				75					80	
Lys	Lys	Thr	Pro	Thr	Ser	Ile	Glu	Tyr	Trp	Phe	Arg	Cys	Met	Asp	Leu
				85				90						95	
Asp	Gly	Asp	Gly	Ala	Leu	Ser	Met	Phe	Glu	Leu	Glu	Tyr	Phe	Tyr	Glu
				100				105					110		
Glu	Gln	Cys	Arg	Arg	Leu	Asp	Ser	Met	Ala	Ile	Glu	Ala	Leu	Pro	Phe
				115				120				125			
Gln	Asp	Cys	Leu	Cys	Gln	Met	Leu	Asp	Leu	Val	Lys	Pro	Arg	Thr	Glu
						135					140				
Gly	Lys	Ile	Thr	Leu	Gln	Asp	Leu	Lys	Arg	Cys	Lys	Leu	Ala	Asn	Val
				145			150			155				160	
Phe	Phe	Asp	Thr	Phe	Phe	Asn	Ile	Glu	Lys	Leu	Asp	His	Glu	Gln	Lys
				165				170					175		
Glu	Gln	Ile	Ser	Leu	Leu	Arg	Asp	Gly	Asp	Ser	Gly	Gly	Pro	Glu	Leu
				180				185					190		
Ser	Asp	Trp	Glu	Lys											
				195											

<210> 105  
 <211> 2264  
 <212> DNA  
 <213> Homo Sapiens

<400> 105

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cgacaacagg gctctattat gaccccaact cgcaatacta ctataattcc ttgaccagag 180
agtaccttta ctgggatggg gaaaaagaga cctacgtgcc agctgcagag tctagctccc 240
accagcagtc gggcctgcct cctgcaaaag aggggaaaga gaagaaggag aaaccaaga 300
gcaaaacagc ccagcagatt gccaaagaca tggaaacgtg ggctaagagt ttgaataagc 360
agaaagaaaa ctttaaaaat agctttcagc ctgtcaattc cttgagggaa gaagaaagga 420
gagaatctgc tgcagcagac gctggccttg ctctctttga gaagaaggga gccttagctg 480
aaaggcagca gctcatccca gaattggtgc gaaatggaga tgaggagaat cccctcaaaa 540
ggggtctggg tgctgcttac agtgggtgaca gtgacaatga ggaggagctg gtggagagac 600
ttgagagtga ggaagagaag ctagctgact ggaagaagat ggcctgtctg ctctgccggc 660
gccagttccc gaacaaagat gccctagtca ggcaccagca actctcagac cttcacaagc 720
aaaacatgga catctaccga cgatccaggc tgagcgagca ggagctggaa gccttggagc 780
taaggagagag agagatgaaa taccgagacc gagctgcaga aagacgggag aagtacggca 840
ttccagaacc tccagagccc aagcgcaaga agcagtttga tgccggcact gtgaattacg 900
agcaaccacac caaagatggc attgaccaca gtaacattgg caacaagatg ctgcaggcca 960
tgggctggcg ggaaggctct ggcttgggac gaaagtgtca aggcattacg gctcccattg 1020
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cgggcgccga ttcctacaaa gatgctgtcc ggaaagccat gtttgccggg ttcactgaga 1140
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gacaccaaag ccacctctgt catttgttgt gatgtctttt cttggcaaaa gccttgtgta 1560
tatttgtata ttacacattt gtacagaatt ttggaagatt ttcaatccaa gttgccaagt 1620
ctggctcctt tacaaaagaa ataccttgag aaaaaaaann aannaaaaaa aanncccnan 1680
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ngtcccaaat nccccaaaa nggagcccn ttaaaattaa angggccgcn nttaaaaaan 1800
nttcngaata nggnaaacc tnggggtttn ccaaatttaa cccctttgaa aaaaaanccc 1860
ctttcncaaa anngggntaa tanccaaaaa gggcccccnn ccatttttgc cntttccaaa 1920
aaaatttgnc caanccnnaa atgggnaaan ggggaatcca atttttttaa gggnnaaaaa 1980
gggtttaaac nnacgggntt ccaaanttgn ttgggggaat ttttaaattc ccaannnccc 2040
aagggggnca atttagnggn cccnaatcc cccaaaaant ggttcnnggn tnaaanngc 2100
cnnnccnnaa tttntanggg tttacttngn tttaaaaaac cccccaaaaa actccccn 2160
gaaccnaaaa aanaaaagga ngccattttt ngngnnaaac ttttttaann nnccnnttaa 2220
angggttaaa aaannnnnnn tnnnccnnaa tttttcaaan aang 2264

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&lt;210&gt; 106

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 106

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Ser Thr Ser Thr Gln Ala Pro Ala Ala Ser Pro Thr Gly Val Val Pro
1          5          10          15
Gly Thr Lys Tyr Ala Val Pro Asp Thr Ser Thr Tyr Gln Tyr Asp Glu
20          25          30
Ser Ser Gly Tyr Tyr Tyr Asp Pro Thr Thr Gly Leu Tyr Tyr Asp Pro
35          40          45
Asn Ser Gln Tyr Tyr Tyr Asn Ser Leu Thr Gln Gln Tyr Leu Tyr Trp
50          55          60
Asp Gly Glu Lys Glu Thr Tyr Val Pro Ala Ala Glu Ser Ser Ser His
65          70          75          80

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Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu  
 85 90 95  
 Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg  
 100 105 110  
 Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe  
 115 120 125  
 Gln Pro Val Asn Ser Leu Arg Glu Glu Glu Arg Arg Glu Ser Ala Ala  
 130 135 140  
 Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu  
 145 150 155 160  
 Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn  
 165 170 175  
 Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn  
 180 185 190  
 Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala  
 195 200 205  
 Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn  
 210 215 220  
 Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln  
 225 230 235 240  
 Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu  
 245 250 255  
 Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala  
 260 265 270  
 Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg  
 275 280 285  
 Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys  
 290 295 300  
 Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met  
 305 310 315 320  
 Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr  
 325 330 335  
 Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala  
 340 345 350  
 Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala  
 355 360 365  
 Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu  
 370 375 380

<210> 107  
 <211> 1367  
 <212> DNA  
 <213> Homo Sapiens

<400> 107

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 gcgaggaacg aggagctacg ggctggggcc cggttattgc catgggcagc ggctgccgca 120  
 tcgaatgcat attcttcagc gagttccacc ccacgctggg acccaagatc acctatcagg 180  
 tccctgaaga cttcatctcc cgagagctgt ttgacacagt ccaagtgtac atcatcacca 240  
 agccagagct gcagaacaag cttatcactg tcacagctat ggaaaagaag ctgatcggtc 300  
 gtcctgtgtg catcgaaacac aagaagtaca gccgcaatgc tctcctcttc aacctgggct 360  
 tcgtgtgtga tgcccaggcc aagacctgag ccctcgagcc cattgttaaa agctgggctg 420  
 gctatctgac cacactagag ctgagagagca gttcgtgtc catggaggag agcaagcaga 480  
 agttgggtgac catcatgacc atcttgctgg aggagctaaa tgcctcaggc cgggtgcactc 540  
 tgcccattga tgagtccaac accatccact tgaagggtgat tgagcagcgg ccagaccctc 600

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cggtggccca ggagtatgat gtacctgtct ttaccaaaga caaggaggat ttcttcaact 660
cacagtggga cctcactaca caacaaatcc tgcctacat tgatgggttc cgcacatcc 720
agaagatttc agcagaggca gatgtggagc tcaacctggt gcgcattgct atccagaacc 780
tgctgtacta cggcgttgtg aacttggtgt ccacctcca gtactccaat gtatactgcc 840
caacgcccac ggtccaggac ctggtagatg acaagtccct gcaagaggca tgtctatcct 900
acgtgaccaa gcaagggcac aagagggccca gtctccggga tgtgtccag ctatactgca 960
gcctgagccc tggcactacc gtgcgagacc tcattggccg ccacccccag cagctgcagc 1020
atgttgatga acggaagctg atccagttcg ggcttatgaa gaacctcatc aggcgactac 1080
agaagtatcc tgtgcgggtg actcgggaag agcagagcca ccctgcccgg ctttatacag 1140
gctgccacag ctatgacgag atctgctgca agacagggcat gagctaccat gagctggatg 1200
agcggcttga aaatgacccc aacatcatca tctgctggaa gtgaggctgg tagtgactgg 1260
atggacacat tgctgtgggt agtccctcct actaggaggc ttgtcatact gtctagaggt 1320
tgactcttag ttctgtaaata aaagacatcc atttcaaaca gccaaaa 1367

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&lt;210&gt; 108

&lt;211&gt; 413

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 108

```

Asp Thr Gly Leu Glu Ala Val Ser Asp Lys Cys Ser Gln Glu Val Gly
1      5      10      15
Thr Pro Leu Arg Glu Glu Arg Gly Ala Thr Gly Leu Gly Pro Val Ile
20     25     30
Ala Met Gly Ser Gly Cys Arg Ile Glu Cys Ile Phe Phe Ser Glu Phe
35     40     45
His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
50     55     60
Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
65     70     75     80
Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
85     90     95
Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
100    105    110
Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
115    120    125
Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
130    135    140
Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
145    150    155    160
Leu Val Pro Ile Met Thr Ile Leu Leu Glu Glu Leu Asn Ala Ser Gly
165    170    175
Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
180    185    190
Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
195    200    205
Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
210    215    220
Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
225    230    235    240
Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
245    250    255
Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
260    265    270
Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val

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275	280	285
Asp Asp Lys Ser Leu Gln Glu Ala Cys Leu Ser Tyr Val Thr Lys Gln		
290	295	300
Gly His Lys Arg Ala Ser Leu Arg Asp Val Phe Gln Leu Tyr Cys Ser		
305	310	315
Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln		
	325	330
Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met		
	340	345
Lys Asn Leu Ile Arg Arg Leu Gln Lys Tyr Pro Val Arg Val Thr Arg		
	355	360
Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr		
	370	375
Asp Glu Ile Cys Cys Lys Thr Gly Met Ser Tyr His Glu Leu Asp Glu		
385	390	395
Arg Leu Glu Asn Asp Pro Asn Ile Ile Ile Cys Trp Lys		
	405	410

<210> 109  
 <211> 2113  
 <212> DNA  
 <213> Homo Sapiens

<400> 109

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tcgatgatgc	cttacagtgc	tactccgaag	ctattaagct	ggatccccac	aaccacgtgc	180
tgtacagcaa	ccgttctgct	gcctatgcca	agaaaggaga	ctaccagaag	gcttatgagg	240
atggctgcaa	gactgtcgac	ctaaagcctg	actggggcaa	gggctattca	cgaaaagcag	300
cagctctaga	gttctttaa	cgctttgaag	aagccaagcg	aacctatgag	gagggcttaa	360
aaacagaggc	aaataaccct	caactgaaag	agggtttaca	gaatatggag	gccagggttg	420
cagagagaaa	attcatgaac	cctttcaaca	tgcctaactc	gtatcagaag	ttggagagtg	480
atcccaggac	aaggacacta	ctcagtgatc	ctacctaccg	ggagctgata	gagcagctac	540
gaaacaagcc	ttctgacctg	ggcacgaaac	tacaagatcc	ccggatcatg	accactctca	600
gcgtcctcct	tggggtcgat	ctgggcagta	tggatgagga	ggaagagatt	gcaacacctc	660
caccaccacc	ccctccaaa	aaggagacca	agccagagcc	aatggaagaa	gatcttccag	720
agaataagaa	gcaggcactg	aaagaaaaag	agctggggaa	cgatgcctac	aagaagaaag	780
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cttacattac	caatcaagca	gcggtatact	ttgaaaaggg	cgactacaat	aagtgccggg	900
agctttgtga	gaaggccatt	gaagtgggga	gagaaaaccg	agaagactat	cgacagattg	960
ccaaagcata	tgctcgaatt	ggcaactcct	acttcaaaga	agaaaagtac	aaggatgcca	1020
tccattttcta	taacaagtct	ctggcagagc	accgaacccc	agatgtgctc	aagaaatgcc	1080
agcaggcaga	gaaaatcctg	aaggagcaag	agcggctggc	ctacataaac	cccgcacctg	1140
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tgaagcatta	tacagaagcc	atcaaaagga	acccgaaaga	tgccaaatta	tacagcaatc	1260
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aacacttaaa	gaatcctgta	atagcacaga	agatccagaa	gctgatggat	gtgggtctga	1680
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ccgccgctgc ctctgggccc tcccagcaca cgcattggctct cttcacccgct gccctcgagt 1920  
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 ttttttattt ggggcagtgg gcatgttatg gggaggggag ggggttcttc cagcctcagg 2040  
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 gcgtggttat aac 2113

<210> 110  
 <211> 543  
 <212> PRT  
 <213> Homo Sapiens

<400> 110  
 Met Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu Ser  
 1 5 10 15  
 Val Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys  
 20 25 30  
 Leu Asp Pro His Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr  
 35 40 45  
 Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr  
 50 55 60  
 Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala  
 65 70 75 80  
 Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu  
 85 90 95  
 Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu  
 100 105 110  
 Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe  
 115 120 125  
 Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg  
 130 135 140  
 Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg  
 145 150 155 160  
 Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met  
 165 170 175  
 Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu  
 180 185 190  
 Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Lys Lys Glu  
 195 200 205  
 Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln  
 210 215 220  
 Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp  
 225 230 235 240  
 Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro  
 245 250 255  
 Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys  
 260 265 270  
 Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val  
 275 280 285  
 Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala  
 290 295 300  
 Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile  
 305 310 315 320  
 His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu  
 325 330 335  
 Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu



340 345 350  
 Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn  
 355 360 365  
 Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr  
 370 375 380  
 Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn Arg  
 385 390 395 400  
 Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp  
 405 410 415  
 Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr  
 420 425 430  
 Arg Lys Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met  
 435 440 445  
 Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala  
 450 455 460  
 Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp  
 465 470 475 480  
 Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln  
 485 490 495  
 Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln  
 500 505 510  
 Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala  
 515 520 525  
 Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg  
 530 535 540

&lt;210&gt; 111

&lt;211&gt; 2765

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 111

gggctgacgac tgacaagcgg ctctgcccgg gaccttctcg ctttcatcta gcgctgcact 60  
 caatggaggg gcgggcaccg cagtgcctta tgctgtctta actagtgtag gaaaacggct 120  
 caaccaccg ctgccgaaat gaagtataag aatcttatgg caagggcctt atatgacaat 180  
 gtcccagagt gtgccgagga actggccttt cgcaagggag acatcctgac cgctcatagag 240  
 cagaacacag ggggactgga aggatggtgg ctgtgctcgt tacacggtcg gcaaggcatt 300  
 gtcccaggca accgggtgaa gcttctgatt ggtcccatgc aggagactgc ctccagtcac 360  
 gagcagcctg cctctggact gatgcagcag acctttggcc aacagaagct ctatcaagt 420  
 ccaaaccac aggtgctcc cggagacacc atctaccaag tgccaccttc ctaccaaatt 480  
 caggaattt accaagtccc cactggccac ggcacccaag aacaagaggt atatcagggtg 540  
 ccaccatcag tgcagagaag cattggggga accagtgggc cccacgtggg taaaaagggtg 600  
 ataacccccg tgaggacagg ccatggctac gtatacagat acccatccag ataccaaaag 660  
 gatgtctatg atatccctcc ttctcatacc actcaagggg tatacgacat cctccctca 720  
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<210> 112  
 <211> 834  
 <212> PRT  
 <213> Homo Sapiens

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<400> 112
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Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu
35          40          45
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile
50          55          60
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
65          70          75          80
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
85          90          95
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr
100         105         110
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu
115         120         125
Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly
130         135         140
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr
145         150         155         160
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
165         170         175
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
180         185         190

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Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile  
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 Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala  
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 Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg  
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 Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly  
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 Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu  
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 Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro  
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 Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro  
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 Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala  
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 Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser  
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 Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His  
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 Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile  
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 Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His  
 485 490 495  
 Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser  
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 Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser  
 565 570 575  
 Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly  
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 Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser  
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 Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser  
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 Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe

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<210> 113
<211> 3429
<212> DNA
<213> Homo. Sapiens
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&lt;210&gt; 114

&lt;211&gt; 906

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 114

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20          25          30
Val Thr Gln Val Thr Thr Leu Val Asn Thr Asn Ser Lys Gly Pro Ser
35          40          45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
50          55          60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65          70          75          80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp

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-82-

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 Asp Asn Tyr Glu Pro Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr  
 565 570 575  
 Lys Leu Leu Ser Asn Thr Val Met Pro Arg Phe Thr Glu Gln Val Glu  
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 Ala Ala Val Glu Ala Leu Ser Ser Asp Pro Ala Gln Pro Met Asp Glu  
 595 600 605  
 Asn Glu Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Ile Arg Asp  
 610 615 620  
 Ile Arg Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Asp Asp  
 625 630 635 640  
 Ser Asp Phe Glu Thr Glu Asp Phe Asp Val Arg Ser Arg Thr Ser Val  
 645 650 655  
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 660 665 670  
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 Ala Ser Phe Gln Glu Glu Lys Ser Lys Leu Asp Ala Glu Val Ser Lys  
 690 695 700  
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 Lys Asn Thr Ser Asp Val Ile Ser Ala Ala Lys Lys Ile Ala Glu Ala  
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 Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro  
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 Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala  
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 Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val  
 785 790 795 800  
 Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met  
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 Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr  
 820 825 830  
 Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly  
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 Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr  
 865 870 875 880  
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<210> 115  
 <211> 1701  
 <212> DNA  
 <213> Homo Sapiens

<400> 115

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&lt;210&gt; 116

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 116

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Met Ala Asn Val Ala Asp Thr Lys Leu Tyr Asp Ile Leu Gly Val Pro
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Ala Gly Ala Ser Glu Asn Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala
20        25        30
Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
35        40        45
Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
50        55        60
Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
65        70        75        80
Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
85        90        95
Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
100       105       110
Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
115       120       125
Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
130       135       140
Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Ser Gly Ala Val Gln Lys

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Cys Ser Ala Cys Arg Gly Arg Gly Val Arg Ile Met Ile Arg Gln Leu						
	165		170		175	
Ala Pro Gly Met Val Gln Gln Met Gln Ser Val Cys Ser Asp Cys Asn						
	180		185		190	
Gly Glu Gly Glu Val Ile Asn Glu Lys Asp Arg Cys Lys Lys Cys Glu						
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Gly Lys Lys Val Ile Lys Glu Val Lys Ile Leu Glu Val His Val Asp						
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Lys Gly Met Lys His Gly Gln Arg Ile Thr Phe Thr Gly Glu Ala Asp						
225		230		235		240
Gln Ala Pro Glu Trp Asn Pro Glu Thr Leu Phe Phe Leu Leu Pro Gly						
	245		250		255	
Glu Lys Asn Met Glu Val Phe Gln Arg Asp Gly Asn Asp Leu His Met						
	260		265		270	
Thr Tyr Lys Ile Gly Leu Val Glu Ala Leu Cys Gly Phe Gln Phe Thr						
	275		280		285	
Leu Ser His Leu Asp Gly Arg Gln Ile Val Val Lys Tyr Pro Pro Gly						
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Lys Val Ile Glu Pro Gly Cys Val Arg Val Val Arg Gly Glu Gly Met						
305		310		315		320
Pro Gln Tyr Arg Asn Pro Phe Glu Lys Gly Gly Leu Tyr Ile Lys Phe						
	325		330		335	
Asp Val Gln Phe Pro Glu Asn Asn Trp Ile Asn Pro Asp Lys Leu Ser						
	340		345		350	
Glu Leu Glu Asp Leu Leu Pro Ser Arg Pro Glu Val Pro Asn Ile Ile						
	355		360		365	
Gly Glu Thr Glu Glu Val Glu Leu Gln Glu Phe Asp Ser Thr Arg Gly						
	370		375		380	
Ser Gly Gly Gly Gln Arg Arg Glu Ala Tyr Asn Asp Ser Ser Asp Glu						
385		390		395		400
Glu Ser Ser Ser His His Gly Pro Gly Val Gln Cys Ala His Gln						
	405		410		415	

<210> 117  
 <211> 1821  
 <212> DNA  
 <213> Homo Sapiens

<400> 117

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agctcttctt agattgacac ctctgtcctt tgaagaaatg ggacactgtg acagtgttta 1080
cctctcagaa gttggagata ctcagtggtt ggtttttaag catgaaaagg aagatggcgc 1140
catttctacc atagtacttc gaggtcttac agacaatctg atggatgaca tagaaagggg 1200
agtagacgat ggtgttaata ctttcaaagt tcttacaagg gataaacgtc ttgtaccggg 1260
aggtggagca acagaaattg aattagccaa acagatcaca tcatatggag agacatgtcc 1320
tggacttgaa cagtatgcta ttaagaagtt tgctgaggca tttgaagcta ttccccgcgc 1380
actggcagaa aactctggag ttaaggccaa tgaagtaatc tctaaacttt atgcagtaca 1440
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catgctggaa gctggtattc tagatactta cctgggaaaa tattgggcta tcaaactcgc 1560
tactaatgct gcagtcactg tacttagagt ggatcagatc atcatggcaa aaccagctgg 1620
tgggccaag cctccaagtg ggaagaaaga ctgggatgat gaccaaaatg attgaaattg 1680
gcttaatttt tactgtaggt gaaggctgta tttgtagtag tactcaagaa tcacctgatg 1740
ttttcttatt ctctttaaata taagagttat tttgtgtttg tattcttggc tggatgttat 1800
aataaacata ttgttactgt c 1821

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&lt;210&gt; 118

&lt;211&gt; 548

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 118

```

Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
1      5      10      15
Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
20     25     30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
35     40     45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
50     55     60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
65     70     75     80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
85     90     95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
100    105    110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
115    120    125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
130    135    140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
145    150    155    160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
165    170    175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
180    185    190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
195    200    205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
210    215    220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
225    230    235    240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
245    250    255

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Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu  
 260 265 270  
 Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala  
 275 280 285  
 Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr  
 290 295 300  
 Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp  
 305 310 315 320  
 Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu  
 325 330 335  
 Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu  
 340 345 350  
 Ser Glu Val Gly Asp Thr Gln Val Val Phe Lys His Glu Lys Glu  
 355 360 365  
 Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu  
 370 375 380  
 Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys  
 385 390 395 400  
 Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu  
 405 410 415  
 Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly  
 420 425 430  
 Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile  
 435 440 445  
 Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile  
 450 455 460  
 Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu  
 465 470 475 480  
 Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly  
 485 490 495  
 Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr  
 500 505 510  
 Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys  
 515 520 525  
 Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp  
 530 535 540  
 Asp Gln Asn Asp  
 545

&lt;210&gt; 119

&lt;211&gt; 1321

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 119

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cccccaagat ggctgctgag gacgagttac agctgccgcg gctccccgag ctgttcgaaa      60
ctggtagaca gttactggac gaagtagaag tggcgactga acccgccggt tcccggatag      120
tccaggagaa ggtgttcaag ggcttgacc tccttgagaa ggctgccgaa atgttatcgc      180
agctcgactt gttcagccga aatgaagatt tggaagagat tgcttcacc gacctgaagt      240
accttttggg gccagcggtt caaggagccc tcaccatgaa acaagtcaac cccagcaagc      300
gtctagatca tttgcagcgg gctcgagaac actttataaa ctacttaact cagtgccatt      360
gctatcatgt ggcagagttt gagctgccca aaaccatgaa caactctgct gaaaatcaca      420
ctgccaatte ctccatggct tatectagtc tcgttgctat ggcattctca agacaggcta      480
aaatacagag atacaagcag aagaaggagt tggagcatag gttgtctgca atgaaatctg      540
ctgtggaaag tggtaagca gatgatgagc gtgttcgtga atattatctt cttcaccttc      600

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agaggtggat tgatatcagc ttagaagaga ttgagagcat tgaccaggaa ataaagatcc 660
tgagagaaag agactcttca agagagggcat caacttctaa ctcactctgc caggagaggc 720
ctccagtga acccttcatt ctactcogga acatggctca agccaaagta tttggagctg 780
gttatccaag tctgccaaact atgacgggtga gtgactggta tgagcaacat cggaaatatg 840
gagcattacc ggatcagggg atagccaagg cagcaccaga ggaattcaga aaagcagctc 900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaaca ctccacagag 960
cccgaggagt ggatgactgg aaggacaccc atcctagggg ctatgggaac cgacagaaca 1020
tgggctgatc tccccacaac accacaggac tgcagggtgc acaactccct gccaaagaaa 1080
accatgcagt cctcccctcc ctggtctcct gcttcagctc tgtacaacga gggcaaagat 1140
gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta 1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc 1260
ttaagtggaa ggaaaagagt gctgagaaat ggctctgtat aatctatggc tatccgaatt 1320
c 1321

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&lt;210&gt; 120

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Homo. Sapiens

&lt;400&gt; 120

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Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
1      5      10     15
Glu Thr Gly Arg Gln Leu Leu Asp Glu Val Glu Val Ala Thr Glu Pro
20     25     30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
35     40     45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
50     55     60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
65     70     75     80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
85     90     95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
100    105    110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
115    120    125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
130    135    140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
145    150    155    160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
165    170    175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
180    185    190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
195    200    205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
210    215    220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
225    230    235    240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
245    250    255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
260    265    270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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275                      280                      285  
 Ala Pro Glu Glu Phe Arg Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu  
 290                      295                      300  
 Glu Lys Glu Glu Glu Asp Asp Glu Gln Thr Leu His Arg Ala Arg Glu  
 305                      310                      315                      320  
 Trp Asp Asp Trp Lys Asp Thr His Pro Arg Gly Tyr Gly Asn Arg Gln  
 325                      330                      335  
 Asn Met Gly

<210> 121  
 <211> 2965  
 <212> DNA  
 <213> Homo Sapiens

<400> 121  
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 ccttagcggt cctctctggg cggcggcggc ggcggctcgg ttgacgcctc ctccgccagc 120  
 tgagcccgcg ggagcccgag acgcccgttc cccgccatc cccgctcccc gaggccggcc 180  
 gcctggtcat ggcgcagccg ggcccggctt cccagcctga cgtttctctt cagcaacggg 240  
 tagcagaatt ggaaaaaatt aatgcagaat ttttacgtgc acaacagcag cttgaacaag 300  
 aatttaataa aaagagagca aaatttaagg agttataatt ggctaaagag gaggatctga 360  
 agaggcaaaa tgagatttta caagctgcac aagatgattt gggacacctt cgaaccacgc 420  
 tgtgggaagc tcaagcagag atggagaata ttaaggcgat tgccacagtc tctgagaaca 480  
 ccaagcaaga agctatagat gaagtgaata gacagtggag agaagaagtt gcttcacttc 540  
 aggtgttat gaaagaaaca gtctgtgact atgagacca gttccacctt aggtggagc 600  
 aggagcgaac acagtgggca cagtatagag aatacgaga gagggaata gctgatttaa 660  
 gaagaagggt gtctgaaggc caagaggagg aaaatttaga aaatgaaatg aaaaaggccc 720  
 aagaggatgc tgagaaactt cggtcctgtg tgatgccaat ggaaaaggaa attgcagctt 780  
 tgaaggataa actgacagag gctgaagaca aaattaaaga gctggaggcc tcaaaggtta 840  
 aagaactgaa tcattatctg gaagctgaga aatctgttag gactgatcta gagatgtatg 900  
 tagctgtttt gaatactcag aaatctgttc tacaggaaga tgctgagaaa ctgaggaaag 960  
 aattgcatga agtttgccat ctcttgagc aagagcgaca acaacacaac cagttaaaac 1020  
 atacgtggca gaaggccaat gaccagtctc tggaatctca gcgtttactg atgagagaca 1080  
 tgacgcgaat ggagattgtg ctaactcag aacagctccg acaagttgaa gaactgaaga 1140  
 agaaagatca ggaggatgat gaacaacaaa gactcaataa gagaaaggat cacaacaaag 1200  
 cagatgttga ggaagaaata aaaataccag tagtgtgtgc tttaactcaa gaagaatctt 1260  
 cagcccagtt atcaaatgaa gaggagcatt tagacagcac ccgtggctca gttcattcct 1320  
 tagatgcagg ctgtgtgtg ccactgtgag atcctttcag taaatcgac aatgacatgt 1380  
 ttaaagatgg actcaggaga gcacagtcta cagacagctt gggaacctcg ggctcattgc 1440  
 aatccaaagc tttaggctat aactacaaag caaaactctg tggaaacctg gacgagtcag 1500  
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 ggtcactcca gatgccaaat gggtttatgt taaccaaaga tcaggaaaga gcaatcaagg 1620  
 cgatgacacc agaacaagaa gagacagcgt ccctcctctc cagcgttacc cagggcatgg 1680  
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 tgcagaaaga ggtacataat gctggaaata aacttggttag acgttgtgat atgtgttcca 1800  
 attacgaaaa acagttacaa ggaattcaga ttcaggaggc tgaaacgaga gaccaggtga 1860  
 aaaaactaca gctgatgcta aggcaagcta atgaccagt agagaagaca atgaaagata 1920  
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 cactcgctct aagagcccag gcctccgaga tcttacttga agagttacag caggggcttt 2040  
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 tgcagtgtgc attacagcaa gcagaagact tcatcctccc agacactaca gaggcactgc 2220  
 gggagttggt attaaaatac cgtgaggaca tcattaatgt gcggacagca gcagaccagc 2280  
 tagaagaaaa gctgaaggct gagatacttt tcctaaaaga gcagatccaa gcagaacagt 2340

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gtttaaaga aaatcttgaa gaaactctgc aactagaaat agaaaactgc aaggaggaaa 2400
tagcttctat ttctagccta aaagctgaat tagaaagaat aaaagtggaa aaaggacagt 2460
tgagagccac attaagagag aagtctcaac agcttgagag tcttcaggaa ataaagatca 2520
gtttggaaga gcagttaaag aaagagactg ctgctaaggc taccgttgaa cagctaattgt 2580
ttgaagagaa gaacaaagct cagagattac agacagaatt agatgtcagt gagcaagtcc 2640
agagagattt tgtaaaagctt tcacagaccc ttcagggtgca gttagagcgg atccggcaag 2700
ctgactcctt ggagagaatc cgggcaattc tgaatgatac taaactgaca gacattaacc 2760
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tcattcttag agcaacagta attattattt aactcttaac tgaagaaaga gaagtcacaa 2880
caaaaggaag actggagaaa tgcttacttc tagagggaga agactgtgcg gcacaggaaa 2940
cagcaaacag tggggtgatc tgcag 2965

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&lt;210&gt; 122

&lt;211&gt; 862

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 122

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Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
 1          5          10          15
Arg Val Ala Glu Leu Glu Lys Ile Asn Ala Glu Phe Leu Arg Ala Gln
      20          25          30
Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu
      35          40          45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
      50          55          60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
      65          70          75          80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
      85          90          95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
      100          105          110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
      115          120          125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
      130          135          140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
      145          150          155          160
Leu Ser Glu Gly Gln Glu Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
      165          170          175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
      180          185          190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
      195          200          205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
      210          215          220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
      225          230          235          240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
      245          250          255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
      260          265          270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
      275          280          285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val

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290	295	300
Leu Thr Ser Glu Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp		
305	310	315
Gln Glu Asp Asp Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys		320
	325	330
Lys Ala Asp Val Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu		335
	340	345
Thr Gln Glu Glu Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu		350
	355	360
Asp Ser Thr Arg Gly Ser Val His Ser Leu Asp Ala Gly Leu Leu Leu		365
	370	375
Pro Ser Gly Asp Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp		380
385	390	395
Gly Leu Arg Arg Ala Gln Ser Thr Asp Ser Leu Gly Thr Ser Gly Ser		400
	405	410
Leu Gln Ser Lys Ala Leu Gly Tyr Asn Tyr Lys Ala Lys Ser Ala Gly		415
	420	425
Asn Leu Asp Glu Ser Asp Phe Gly Pro Leu Val Gly Ala Asp Ser Val		430
	435	440
Ser Glu Asn Phe Asp Thr Ala Ser Leu Gly Ser Leu Gln Met Pro Ser		445
	450	455
Gly Phe Met Leu Thr Lys Asp Gln Glu Arg Ala Ile Lys Ala Met Thr		460
465	470	475
Pro Glu Gln Glu Glu Thr Ala Ser Leu Leu Ser Ser Val Thr Gln Gly		480
	485	490
Met Glu Ser Ala Tyr Val Ser Pro Ser Gly Tyr Arg Leu Val Ser Glu		495
	500	505
Thr Glu Trp Asn Leu Leu Gln Lys Glu Val His Asn Ala Gly Asn Lys		510
	515	520
Leu Gly Arg Arg Cys Asp Met Cys Ser Asn Tyr Glu Lys Gln Leu Gln		525
	530	535
Gly Ile Gln Ile Gln Glu Ala Glu Thr Arg Asp Gln Val Lys Lys Leu		540
545	550	555
Gln Leu Met Leu Arg Gln Ala Asn Asp Gln Leu Glu Lys Thr Met Lys		560
	565	570
Asp Lys Gln Glu Leu Glu Asp Phe Ile Lys Gln Ser Ser Glu Asp Ser		575
	580	585
Ser His Gln Ile Ser Ala Leu Val Leu Arg Ala Gln Ala Ser Glu Ile		590
	595	600
Leu Leu Glu Glu Leu Gln Gln Gly Leu Ser Gln Ala Lys Arg Asp Val		605
	610	615
Gln Glu Gln Met Ala Val Leu Met Gln Ser Arg Glu Gln Val Ser Glu		620
625	630	635
Glu Leu Val Arg Leu Gln Lys Asp Asn Asp Ser Leu Gln Gly Lys His		640
	645	650
Ser Leu His Val Ser Leu Gln Gln Ala Glu Asp Phe Ile Leu Pro Asp		655
	660	665
Thr Thr Glu Ala Leu Arg Glu Leu Val Leu Lys Tyr Arg Glu Asp Ile		670
	675	680
Ile Asn Val Arg Thr Ala Ala Asp His Val Glu Glu Lys Leu Lys Ala		685
	690	695
Glu Ile Leu Phe Leu Lys Glu Gln Ile Gln Ala Glu Gln Cys Leu Lys		700
705	710	715
Glu Asn Leu Glu Glu Thr Leu Gln Leu Glu Ile Glu Asn Cys Lys Glu		720
	725	730
		735

Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys  
                     740                    745                    750  
 Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln  
                     755                    760                    765  
 Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys  
                     770                    775                    780  
 Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu  
                     785                    790                    795                    800  
 Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln  
                     805                    810                    815  
 Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu  
                     820                    825                    830  
 Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu  
                     835                    840                    845  
 Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr  
                     850                    855                    860

<210> 123  
 <211> 544  
 <212> DNA  
 <213> Homo Sapiens

<400> 123  
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 ttggtttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa 180  
 atgaagtaga aaaggttaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa 240  
 atgacaatta tagaacaacg ggaattgcta caatcgaggt gtttttacc ccaagactaa 300  
 aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt 360  
 ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga 420  
 agcaactacn actaggggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga 480  
 tgggtgcttga actaaaacaa tctgaagagg acgcgaggaa aaacttcag ttagaggaag 540  
 agga 544

<210> 124  
 <211> 178  
 <212> PRT  
 <213> Homo Sapiens

<400> 124  
 Glu Trp Arg Gly Ala Gly Met Ala Gln Lys Lys Tyr Leu Gln Ala Lys  
   1                    5                    10                    15  
 Leu Thr Gln Phe Leu Arg Glu Asp Arg Ile Gln Leu Trp Lys Pro Pro  
                     20                    25                    30  
 Tyr Thr Asp Glu Asn Lys Lys Val Gly Leu Ala Leu Lys Asp Leu Ala  
                     35                    40                    45  
 Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys  
                     50                    55                    60  
 Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn  
   65                    70                    75                    80  
 Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro  
                     85                    90                    95  
 Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His  
                     100                    105                    110  
 Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu



115                      120                      125  
 Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys  
 130                      135                      140  
 Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu  
 145                      150                      155                      160  
 Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu  
 165                      170                      175  
 Glu Glu

<210> 125  
 <211> 1302  
 <212> DNA  
 <213> Homo Sapiens

<400> 125  
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 aagcgggcca agctcatcgg caagtacctg atgggggacc tgctggggga aggtctttac 180  
 ggcaaggtga aggaggtgct ggactcggag acgctgtgca ggagggccgt caagatcctc 240  
 aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa 300  
 ctactgagga ggttacggca caaaaatgtc atccagctgg tggatgtgtt atacaacgaa 360  
 gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg 420  
 gacagcgtgc cggagaagcg tttcccagtg tgccaggccc acgggtactt ctgtcagctg 480  
 attgacggcc tggagtagct gcatagccag ggcattgtgc acaaggacat caagccgggg 540  
 aacctgctgc tcaccaccgg tggcaccctc aaaatctccg acctgggcgt ggccgaggca 600  
 ctgcaccctg tcgcggcgga cgacacctgc cggaccagcc agggctcccc ggctttccag 660  
 ccgcccgaga ttgccaacgg cctggacacc ttctccggct tcaagtgga catctggtcg 720  
 gctgggggtca ccctctacaa catcaccacg ggtctgtacc ccttcgaagg ggacaacatc 780  
 tacaagttgt ttgagaacat cgggaagggg agctacgcca tcccgggcga ctgtggcccc 840  
 ccgctctctg acctgctgaa agggatgctt gagtacgaac cggccaagag gttctccatc 900  
 cggcagatcc ggcagcacag ctggttccgg aagaaacatc ctccggctga agcaccagt 960  
 cccatccac cgagcccgga caccaaggac cgggtggcga gcatgactgt ggtgccgtac 1020  
 ttggaggacc tgcacggcgc ggacgaggac gaggacctct tcgacatcga ggatgacatc 1080  
 atctacactc aggacttcac ggtgcccgga caggtcccag aagaggaggc cagtcacaat 1140  
 ggacagcgcc ggggcctccc caaggccgtg tgtatgaacg gcacagaggc ggcgagctg 1200  
 agcaccaaat ccaggcgga gggccgggccc cccaacctg cccgcaaggc ctgctccgcc 1260  
 agcagcaaga tccgcgggct gtcggcctgc aagcagcagt ga 1302

<210> 126  
 <211> 433  
 <212> PRT  
 <213> Homo Sapiens

<400> 126  
 Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu  
 1                      5                      10                      15  
 Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr  
 20                      25                      30  
 Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys  
 35                      40                      45  
 Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys  
 50                      55                      60  
 Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu  
 65                      70                      75                      80

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys  
 85 90 95  
 Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln  
 100 105 110  
 Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val  
 115 120 125  
 Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro  
 130 135 140  
 Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu  
 145 150 155 160  
 Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp  
 165 170 175  
 Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile  
 180 185 190  
 Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp  
 195 200 205  
 Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile  
 210 215 220  
 Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser  
 225 230 235 240  
 Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu  
 245 250 255  
 Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr  
 260 265 270  
 Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly  
 275 280 285  
 Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg  
 290 295 300  
 Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val  
 305 310 315 320  
 Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr  
 325 330 335  
 Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp  
 340 345 350  
 Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val  
 355 360 365  
 Pro Gly Gln Val Pro Glu Glu Glu Ala Ser His Asn Gly Gln Arg Arg  
 370 375 380  
 Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu  
 385 390 395 400  
 Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys  
 405 410 415  
 Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln  
 420 425 430  
 Gln

<210> 127  
 <211> 1488  
 <212> DNA  
 <213> Homo Sapiens

<400> 127  
 gaggggcccgg gcggtgccgg caagatggct ggcgccgaga agatgacgtt tcccagagaaa  
 ccaagccaca aaaagtacag ggccgccctg aagaaggaga aacgaaagaa acgtcggcag

60  
 120

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gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt 180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat 240
gaggagtggg tgctaagaga gcagaaggca caagaagaat tcagaataaa gaagggaaaag 300
gaagaggcgg ctaaaaaacg gcaagaagaa caagagagaa agttaaaagga acaatgggaa 360
gaacagcaga ggaaagagag agaagaggag gacagaaaac gacaggagaa gaaagaaaaa 420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tgggtaccaca 480
tggcaaaaacc cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt 540
cccttctaca gtaaaacagg agcttgacga tttggagata gatgttcacg taaacataat 600
ttcccaacat ccagtcctac ccttcttatt aagagcatgt ttacgacgtt tggaatggag 660
cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc 720
taccaacagt tcctagactt ctatgaggat gtgttgcccg agttcaagaa cgtggggaaa 780
gtgattcagt tcaaggtcag ctgcaatttg gaacctcacc tgaggggcaa tgtatatgtt 840
cagtaccagt cggaagaaga atgccaagca gccctttctc tgtttaacgg acgatgggtat 900
gcaggacgac agctgcagtg tgaattctgc cccgtgaccc ggtggaaaat ggcgatttgt 960
ggtttatttg aaatacaaca atgtccaaga ggaaagcact gcaactttct tcatgtgttc 1020
agaaatccca acaatgaatt ctgggaagct aatagagaca tctactgtc tccagatcgg 1080
actggctcct cctttgggaa gaactccgaa aggagggaga ggatgggcca ccacgacgac 1140
tactacagca ggctgcgggg aaggagaaac cctagtccag accactccta caaaagaaat 1200
ggggaatccg agaggaaaag tagtcgtcac agggggaaga aatctcacia acgcacatca 1260
aagagtcggg agaggcacia ttcacgaagc agaggaagaa atagggaccg cagcagggac 1320
cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccgc 1380
agccggagcc aaagttctc taggtcccga agtcgtggca ggaggaggtc gggtaataga 1440
gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt 1488

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&lt;210&gt; 128

&lt;211&gt; 482

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 128

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Met Ala Ala Pro Glu Lys Met Thr Phe Pro Glu Lys Pro Ser His Lys
1          5          10          15
Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg Gln
20          25          30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
35          40          45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu Leu
50          55          60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
65          70          75          80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
85          90          95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
100          105          110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Glu Gln Lys Arg Gln Glu
115          120          125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
130          135          140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
145          150          155          160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
165          170          175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
180          185          190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr

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195	200	205
Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser		
210	215	220
Leu Glu Tyr Ser Glu Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr		
225	230	235
Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe		
245	250	255
Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val		
260	265	270
Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn		
275	280	285
Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val		
290	295	300
Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys		
305	310	315
Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn		
325	330	335
Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg		
340	345	350
Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly		
355	360	365
His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser		
370	375	380
Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser		
385	390	395
Arg His Arg Gly Lys Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu		
405	410	415
Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp		
420	425	430
Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg		
435	440	445
Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg		
450	455	460
Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys		
465	470	475
480		
Ser Lys		

<210> 129  
 <211> 1663  
 <212> DNA  
 <213> Homo Sapiens

<400> 129	
aggccttgag ccaactccgg gtgctctgct gtgagtggct gaggcccag atccacacca	60
aggagcagat cctggagcta ctggtgctgg agcagttcct gaccatectg ccccaggagc	120
tccaggcctg ggtgcaggag cattgcccgg agagcgctga agaggctgtc actctctctg	180
aagatctgga gcgggaactg gatgagccag gacaccaggt ctcaactcct ccaaacgaac	240
agaaaccggt gtgggagaag atatcctcct caggaactgc aaaggaatcc ccgagcagca	300
tgcagccaca gcccttgagg accagtcaca aatacagatc ttgggggccc ctgtacatcc	360
aagagtctgg tgaggagcag gagttcgctc aagatccaag aaaggtccga gattgcagat	420
tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gaggggctca	480
aaggggatat aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt	540
gcgtaaacct tgaaaatgaa aaaggaacaa aacccctct tcaagaggca ggctccaaga	600
aaggtagaga atcagttcct actaaacctt ccccaggaga gagacgttat atatgtgctg	660

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aatgtggcaa agccttttagt aatagctcaa atctcaccaa acacaggaga acacacactg 720
gggagaaaacc ttacgtgtgc accaagtgtg ggaaagcttt cagccacagc tcaaacctca 780
ccctccacta cagaacacac ttggtggacc ggccctatga ctgtaagtgt ggaaaagctt 840
ttgggcagag ctcagacctt cttaaaccatc agagaatgca cacagaagag gcgccatata 900
agtggcaaaga ttgtggcaag gctttcagcg ggaaaggcag cctcattcgt cactatcgga 960
tccacactgg ggagaagcct tatcagtgtg acgaatgtgg gaagagcttc agtcagcatg 1020
cgggcctcag ctcccaccag agactccaca ccggagagaa gccatataag tgtaaggagt 1080
gtgggaaagc cttcaaccac agctccaact tcaataaaca ccacagaatc cacaccgggg 1140
aaaagcccta ctggtgtcat cactgtggaa agaccttctg tagcaagtcc aatctttcca 1200
aacatcagcg agtccacact ggagagggag aagcaccgta actttcaagc gctcctgttg 1260
ttgtcgttgt tttaaacttt agaactctgaa aaccagaaaag aagtcttgtc attgcagcag 1320
catcgattcc ggtgatagag tttgtatcac tcaacatcag gggatgcctg aggagtgcga 1380
gctccacagc aacatggcag gcaggagggt ctcagaagggt gtcaggagggt tccacactcg 1440
ccagttcact ggagcagagt cccttcgcca cacttaggggt cccagtaagc catgccagca 1500
ttaccctttg cgtagttaaa cagacgtgta tccagtctag ttaaggaaga aacattaaga 1560
ttgtttaatt tttacatat attcaagaat ttttaattgt aaagaattga gccacattga 1620
acacaattga atgagattca gaataaactt ataacatctt aaa 1663

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&lt;210&gt; 130

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 130

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Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp Leu Arg Pro Glu
1      5      10      15
Ile His Thr Lys Glu Gln Ile Leu Glu Leu Val Leu Glu Gln Phe
20     25     30
Leu Thr Ile Leu Pro Gln Glu Leu Gln Ala Trp Val Gln Glu His Cys
35     40     45
Pro Glu Ser Ala Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu Arg
50     55     60
Glu Leu Asp Glu Pro Gly His Gln Val Ser Thr Pro Pro Asn Glu Gln
65     70     75     80
Lys Pro Val Trp Glu Lys Ile Ser Ser Ser Gly Thr Ala Lys Glu Ser
85     90     95
Pro Ser Ser Met Gln Pro Gln Pro Leu Glu Thr Ser His Lys Tyr Glu
100    105    110
Ser Trp Gly Pro Leu Tyr Ile Gln Glu Ser Gly Glu Glu Gln Glu Phe
115    120    125
Ala Gln Asp Pro Arg Lys Val Arg Asp Cys Arg Leu Ser Thr Gln His
130    135    140
Glu Glu Ser Ala Asp Glu Gln Lys Gly Ser Glu Ala Glu Gly Leu Lys
145    150    155    160
Gly Asp Ile Ile Ser Val Ile Ile Ala Asn Lys Pro Glu Ala Ser Leu
165    170    175
Glu Arg Gln Cys Val Asn Leu Glu Asn Glu Lys Gly Thr Lys Pro Pro
180    185    190
Leu Gln Glu Ala Gly Ser Lys Lys Gly Arg Glu Ser Val Pro Thr Lys
195    200    205
Pro Thr Pro Gly Glu Arg Arg Tyr Ile Cys Ala Glu Cys Gly Lys Ala
210    215    220
Phe Ser Asn Ser Ser Asn Leu Thr Lys His Arg Arg Thr His Thr Gly
225    230    235    240
Glu Lys Pro Tyr Val Cys Thr Lys Cys Gly Lys Ala Phe Ser His Ser

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245 250 255  
 Ser Asn Leu Thr Leu His Tyr Arg Thr His Leu Val Asp Arg Pro Tyr  
 260 265 270  
 Asp Cys Lys Cys Gly Lys Ala Phe Gly Gln Ser Ser Asp Leu Leu Lys  
 275 280 285  
 His Gln Arg Met His Thr Glu Glu Ala Pro Tyr Gln Cys Lys Asp Cys  
 290 295 300  
 Gly Lys Ala Phe Ser Gly Lys Gly Ser Leu Ile Arg His Tyr Arg Ile  
 305 310 315 320  
 His Thr Gly Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Ser Phe  
 325 330 335  
 Ser Gln His Ala Gly Leu Ser Ser His Gln Arg Leu His Thr Gly Glu  
 340 345 350  
 Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn His Ser Ser  
 355 360 365  
 Asn Phe Asn Lys His His Arg Ile His Thr Gly Glu Lys Pro Tyr Trp  
 370 375 380  
 Cys His His Cys Gly Lys Thr Phe Cys Ser Lys Ser Asn Leu Ser Lys  
 385 390 395 400  
 His Gln Arg Val His Thr Gly Glu Gly Glu Ala Pro  
 405 410

<210> 131  
 <211> 724  
 <212> DNA  
 <213> Homo Sapiens

<400> 131  
 ggagaatgaa aagcagaaag tggcagagct gtattctatc cataactctg gagacaaatc 60  
 tgatattcag gacctctctg agagtgtcag gctggacaaa gaaaaagcag agactttggc 120  
 tagtagcttg caggaagatc tggctcatc ccgaaatgat gccaatcgat tacaggatgc 180  
 cattgctaag gtagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga 240  
 agatttgaat atgacgttag aaaaattaag atcagacctg gatgaaaaag aaacagaaag 300  
 gagtgacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt 360  
 gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga 420  
 ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc 480  
 tgcggaatgg cggcagtttc aggtgatct ccagactgca gtagtcattg caaatgacat 540  
 taaatctgaa gcccaagagg agattggtga tctaaagcgc cgggtacatg aggtcaaga 600  
 aaaaaatgag aaactcacia aagaattgga ggaaataagt ccgccaagcc agaagangac 660  
 gangccggtg ttccantaca tgnatgcccg tgagagagaa tttggcaggc ctaaggcag 720  
 ggaa 724

<210> 132  
 <211> 218  
 <212> PRT  
 <213> Homo Sapiens

<400> 132  
 Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser  
 1 5 10 15  
 Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp  
 20 25 30  
 Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala  
 35 40 45  
 His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val

50                      55                      60  
 Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu  
 65                      70                      75                      80  
 Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys  
                     85                      90                      95  
 Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp  
                     100                      105                      110  
 Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile  
                     115                      120                      125  
 Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp  
                     130                      135                      140  
 Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser  
 145                      150                      155                      160  
 Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile  
                     165                      170                      175  
 Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys  
                     180                      185                      190  
 Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu  
                     195                      200                      205  
 Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys  
 210                      215

<210> 133  
 <211> 719  
 <212> DNA  
 <213> Homo Sapiens

<400> 133  
 gagaactaca gagctgggtg cggggccaac ggccagaaag tggcgaggag gcagtgcgc 60  
 tgggtggaggg tttgcagaaa caaccagga gaccaaggcg gtgactgtcc atgttcacgg 120  
 ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaata 180  
 gctgcaggat cctgtgcaaa gctcgacccc cgagcagtc cctgaggaaa ccacacagag 240  
 cccagatctg ggggcaccgg cagagcagcg tccacaccag gaagaggagc tccagaccct 300  
 gcaggagagc gaggtcccag tgcccagga cccagacctt cctgcagaga ggagctctgg 360  
 agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga 420  
 tgtggccgta tgcttttccc aggaccagtg gactgatctg gacccaacac agaaagagtt 480  
 ctatggagaa tatgtcttgg aagaagactg tggaattggt gtctctctgt catttccaat 540  
 cccagacct gatgagatct cccagggttag agaggaagag cccttgggtc ccagatatcc 600  
 aagagcctna ggagactcaa gagccagaaa tcctgagttt tacctacaca ggagatagga 660  
 gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca 719

<210> 134  
 <211> 217  
 <212> PRT  
 <213> Homo Sapiens

<400> 134  
 Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly  
 1                      5                      10                      15  
 Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys  
                     20                      25                      30  
 Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr  
                     35                      40                      45  
 Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro  
 50                      55                      60

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser  
 65 70 75 80  
 Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu  
 85 90 95  
 Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp  
 100 105 110  
 Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu  
 115 120 125  
 Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys  
 130 135 140  
 Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe  
 145 150 155 160  
 Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu  
 165 170 175  
 Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu  
 180 185 190  
 Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg  
 195 200 205  
 Asn Pro Glu Phe Tyr Leu His Arg Arg  
 210 215

<210> 135  
 <211> 1027  
 <212> DNA  
 <213> Homo Sapiens

<400> 135  
 gcgaggcg gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60  
 actacgacgc cggcaggtac agcccgcggc tgctcacggc gcacgagctg ccactggacg 120  
 cgcacgtgct ggaaccggat gaggacctgc agcgcccgca gctctcggcg cagcagctcc 180  
 aggtcacggg agacgccagc gagagcgccg aggacatctt cttccggcgg gccaaaggagg 240  
 gcatgggcca ggacgaggcg cagttcagcg tggagatgcc actcaccggc aaggcctacc 300  
 tgtgggcca caagtaccgg ccacgcaagc cgcgcttctt caaccgcgtg cacacgggct 360  
 tcgagtggaa caagtacaac cagacgcact acgactttga caaccaccg cccaagatcg 420  
 tgcagggata caagttcaac atcttctacc ccgacctcat cgacaagcgc tccacgcccg 480  
 agtacttcct ggaggcctgc gccgacaaca aggatttcgc catcctgcgc ttcacgcggg 540  
 gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtgggaata ctngcaccgc 600  
 cacggcttcc gctgccagtt tgccaacggc attttccanc tgngetttca cttcaagcgc 660  
 tnccgctatc ggcgggtgacg gccctgggga acggcaggcc aggagggcg agggccacac 720  
 ggggtgccaca gcccaggctc gagtggccca gccggcaggc ttgtttttca gcatccgacg 780  
 ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccacca 840  
 acctcaccag tcaccagccc cagaccaccc acagcccctc ccagacaccc cgcctcatct 900  
 ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaa atcttttggt 960  
 ctcatggaat tggcctattg gcaagatcgc atgttttttt aataaacggt gtattttaga 1020  
 ataaaaa 1027

<210> 136  
 <211> 299  
 <212> PRT  
 <213> Homo Sapiens

<400> 136  
 Glu Gly Glu Gly Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln  
 1 5 10 15  
 Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr



Ala	His	Glu	Leu	Pro	Leu	Asp	Ala	His	Val	Leu	Glu	Pro	Asp	Glu	Asp
35							40						45		
Leu	Gln	Arg	Leu	Gln	Leu	Ser	Arg	Gln	Gln	Leu	Gln	Val	Thr	Gly	Asp
50						55					60				
Ala	Ser	Glu	Ser	Ala	Glu	Asp	Ile	Phe	Phe	Arg	Arg	Ala	Lys	Glu	Gly
65					70					75				80	
Met	Gly	Gln	Asp	Glu	Ala	Gln	Phe	Ser	Val	Glu	Met	Pro	Leu	Thr	Gly
				85					90					95	
Lys	Ala	Tyr	Leu	Trp	Ala	Asp	Lys	Tyr	Arg	Pro	Arg	Lys	Pro	Arg	Phe
			100					105					110		
Phe	Asn	Arg	Val	His	Thr	Gly	Phe	Glu	Trp	Asn	Lys	Tyr	Asn	Gln	Thr
	115						120						125		
His	Tyr	Asp	Phe	Asp	Asn	Pro	Pro	Pro	Lys	Ile	Val	Gln	Gly	Tyr	Lys
	130					135					140				
Phe	Asn	Ile	Phe	Tyr	Pro	Asp	Leu	Ile	Asp	Lys	Arg	Ser	Thr	Pro	Glu
145					150					155					160
Tyr	Phe	Leu	Glu	Ala	Cys	Ala	Asp	Asn	Lys	Asp	Phe	Ala	Ile	Leu	Arg
				165					170					175	
Phe	Thr	Arg	Gly	Arg	Leu	Arg	Gly	His	Arg	Phe	Gln	Asp	Arg	Gln	Pro
			180					185					190		
Arg	Val	Gly	Ile	Leu	Ala	Pro	Pro	Arg	Leu	Pro	Leu	Pro	Val	Cys	Gln
	195						200						205		
Arg	His	Phe	Pro	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Leu	Ser	Ala	Val	Thr
	210					215						220			
Ala	Leu	Gly	Asn	Gly	Arg	Pro	Gly	Gly	Pro	Arg	Ala	Thr	Arg	Val	Pro
225					230					235					240
Gln	Pro	Arg	Ser	Glu	Trp	Pro	Ser	Arg	Gln	Ala	Cys	Phe	Ser	Ala	Ser
				245					250					255	
Asp	Gly	Asn	Ile	Ser	Asn	Arg	Ser	Lys	Thr	Glu	Ser	Ala	Ser	Arg	Thr
	260							265					270		
Pro	Arg	Gly	Pro	Pro	Asn	Leu	Thr	Ser	His	Gln	Pro	Gln	Thr	Thr	His
	275						280						285		
Ser	Pro	Ser	Gln	Thr	Pro	Arg	Leu	Ile	Trp	Lys					
	290						295								

<210> 137  
 <211> 766  
 <212> DNA  
 <213> Homo Sapiens

<400> 137

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ttggaaggcc	gaaagagctg	acgattagaa	cacagaagtt	taaagcaatg	ttgtggatgt	300
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gaacgagtgc	tcattttgca	agactgagag	atttcatcaa	attggaattc	ccacctggat	420
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<210> 138  
 <211> 243  
 <212> PRT  
 <213> Homo Sapiens

<400> 138  
 Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr  
 1 5 10 15  
 Glu His Leu Thr Glu Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro  
 20 25 30  
 Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly  
 35 40 45  
 Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr  
 50 55 60  
 Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile  
 65 70 75 80  
 Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met  
 85 90 95  
 Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile  
 100 105 110  
 Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu  
 115 120 125  
 Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile  
 130 135 140  
 Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile  
 145 150 155 160  
 Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln  
 165 170 175  
 Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu  
 180 185 190  
 Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly  
 195 200 205  
 Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu  
 210 215 220  
 Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg  
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 Asp Pro Phe

<210> 139  
 <211> 3060  
 <212> DNA  
 <213> Homo Sapiens

<400> 139  
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 ggcgggcatt gttcgcgcgc gccgcgcgcg cgcggggcca tgggggcccgc ccggcgcccgc 360  
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cgcttccgca tgatctacct gcagacgttg ctggccaagg aaaagaagag ctatgaccgg 660
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gagcgtgcag agtggaggga gaacatccg gagcagcaga agaagtgtt cagaagcttc 3060

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&lt;210&gt; 140

&lt;211&gt; 872

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 140

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Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
 1             5             10            15
Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
          20            25            30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
          35            40            45
Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala

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50	55	60
Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala		
65	70	75
Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg		80
	85	90
Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu		95
	100	105
Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro		110
	115	120
Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp		125
	130	135
Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg		140
	145	150
Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe		155
	165	170
Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn		175
	180	185
Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met		190
	195	200
Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly		205
	210	215
Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys		220
	225	230
Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu		235
	245	250
Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro		255
	260	265
Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met		270
	275	280
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu		285
	290	295
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser		300
	305	310
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu		315
	325	330
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg		335
	340	345
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg		350
	355	360
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro		365
	370	375
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser		380
	385	390
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn		395
	405	410
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr		415
	420	425
Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg		430
	435	440
His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro		445
	450	455
His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly		460
	465	470
Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu		475
	485	490
		495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr  
 500 505 510  
 Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys  
 515 520 525  
 Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu  
 530 535 540  
 Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe  
 545 550 555 560  
 Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg  
 565 570 575  
 Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg  
 580 585 590  
 Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys  
 595 600 605  
 Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala  
 610 615 620  
 Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu  
 625 630 635 640  
 Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val  
 645 650 655  
 Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro  
 660 665 670  
 Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile  
 675 680 685  
 Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly  
 690 695 700  
 Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu  
 705 710 715 720  
 Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu  
 725 730 735  
 Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp  
 740 745 750  
 Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp  
 755 760 765  
 Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu  
 770 775 780  
 Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg  
 785 790 795 800  
 Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys  
 805 810 815  
 Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Met Ser Pro Ser Met  
 820 825 830  
 Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile  
 835 840 845  
 Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln  
 850 855 860  
 Gln Lys Lys Cys Phe Arg Ser Phe  
 865 870

&lt;210&gt; 141

&lt;211&gt; 691

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 141

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ccccttcttt cctttccact cccccagccg cctctttgac cagttcttcg gagagcacct 120
gttgaggtct gatcttttcc cgacgtctac ttccctgagt cccttctacc ttcggccacc 180
ctccttcttg cgggcaccca gctggtttga cactggactc tcagagatgc gcctggagaa 240
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cattacttca tccctgtcat ctgatggggt cctcactgtg aatggaccaaa ggaaacaggt 480
ctctggccct gagcgcacca ttcccatcac ccgtgaagag aagcctgctg tcaccgcagc 540
cccccaagaaa tagatgccct ttcttgaatt gcatttttta aaacaagaaa gtttccccac 600
cagtgaatga aagtcttggt actagtgtg aagcttatta atgctaaggg caggcccaaa 660
ttatcaagct aataaaatat cattcagcaa c 691

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&lt;210&gt; 142

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 142

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Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
1           5           10          15
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
20          25          30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
35          40          45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
50          55          60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65          70          75          80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
85          90          95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
100         105         110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
115         120         125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
130         135         140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145         150         155         160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
165         170         175

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&lt;210&gt; 143

&lt;211&gt; 1300

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 143

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cagacttggg atcagttata aactctagag tgcttactgc agtgcattgg attcagtcag 360
cttttgatga agctatgtca tactgtogat atcatccttc caaagggtat tgggtggcact 420

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actggacaaa	agagaagcct	ggaagactcc	tcagtctagt	tatcatacct	cagtactgtg	780
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&lt;210&gt; 144

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 144

Leu	Leu	Gly	Ile	Ser	Trp	Val	Asp	Ser	Ser	Trp	Ile	Pro	Ile	Leu	Asn
1				5					10					15	
Ser	Gly	Ser	Val	Leu	Asp	Tyr	Phe	Ser	Glu	Arg	Ser	Asn	Pro	Phe	Tyr
			20					25				30			
Asp	Arg	Thr	Cys	Asn	Asn	Glu	Val	Val	Lys	Met	Gln	Arg	Leu	Thr	Leu
		35					40					45			
Glu	His	Leu	Asn	Gln	Met	Val	Gly	Ile	Glu	Tyr	Ile	Leu	Leu	His	Ala
	50					55					60				
Gln	Glu	Pro	Ile	Leu	Phe	Ile	Ile	Arg	Lys	Gln	Gln	Arg	Gln	Ser	Pro
	65				70				75					80	
Ala	Gln	Val	Ile	Pro	Leu	Ala	Asp	Tyr	Tyr	Ile	Ile	Ala	Gly	Val	Ile
			85					90					95		
Tyr	Gln	Ala	Pro	Asp	Leu	Gly	Ser	Val	Ile	Asn	Ser	Arg	Val	Leu	Thr
		100					105					110			
Ala	Val	His	Gly	Ile	Gln	Ser	Ala	Phe	Asp	Glu	Ala	Met	Ser	Tyr	Cys
	115					120						125			
Arg	Tyr	His	Pro	Ser	Lys	Gly	Tyr	Trp	Trp	His	Phe	Lys	Asp	His	Glu
	130					135					140				
Glu	Gln	Asp	Lys	Val	Arg	Pro	Lys	Ala	Lys	Arg	Lys	Glu	Glu	Pro	Ser
	145			150				155						160	
Ser	Ile	Phe	Gln	Arg	Gln	Arg	Val	Asp	Ala	Leu	Leu	Leu	Asp	Leu	Arg
			165				170						175		
Gln	Lys	Phe	Pro	Pro	Lys	Phe	Val	Gln	Leu	Lys	Pro	Gly	Glu	Lys	Pro
		180					185					190			
Val	Gln	Val	Asp	Gln	Thr	Lys	Lys	Glu	Ala	Glu	Pro	Ile	Pro	Glu	Thr
	195					200						205			
Val	Lys	Pro	Glu	Glu	Lys	Glu	Thr	Pro	Glu	Cys	Thr	Thr	Arg	Pro	Gly
	210				215						220				
Val	Leu	Lys	Ala	Pro	Leu	Lys	Asn	Gly							
	225				230										

&lt;210&gt; 145

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 145

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gcggccaaact ccaatgggccc tttccagccc gtggtccttc tccatattcg agatgttcct      180
cctgctgatac aagagaagct ttttatccag aagttacgtc agtggtgcgt cctctttgac      240
tttgtttctg atccactaag tgacctaaag tgggaaggaag taaaacgagc tgctttaagt      300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttaccagaa      360
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gcgaagaaat atattgatca gaagtttgta ttgcagcttt tagagctctt tgacagtga      600
gatcctcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta      660
ggcttgagag cttacatcag aaaacagata aataatatat tttatagggt tatttatgaa      720
acagagcatc ataatggcat agcagagtta ctggaaatat tgggaagtat aattaatgga      780
tttgccttac cactaaaaga agagcacaag attttcttat tgaagggtgt actacctttg      840
cacaaagtga aatctctgag tgtctacat cccagctgg catactgtgt agtgcagttt      900
ttagaaaagg acagcacctc cacggaacca gtggtgatgg cacttctcaa atactggcca      960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat ttagatgtc     1020
attgaaccat cagaatttgt gaagatcatg gaacccctct tccggcagtt ggccaaatgt     1080
gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac     1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tccttccttg     1200
taccgcaact caaagaccca ttggaacaag acaatacatg gcttgatata caacgcctg      1260
aagctcttca tggagatgaa ccaaaagcta tttgatgact gtacacaaca gttcaaagca      1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa      1380
aatctagcca aagccaatcc ccaggtacta aaaaagagaa taacatgaaa aggcpcaggg      1440
ttacttgaat gtttttataa gataggaata tatgtcttca ccatgggggg ggtctcgatt     1500
tcactaacgt tgtatatgaa aatgtctg                                     1528

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&lt;210&gt; 146

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 146

```

Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
 1              5              10              15
Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
      20              25              30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
      35              40              45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
      50              55              60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
      65              70              75              80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
      85              90              95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
      100             105             110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
      115             120             125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Phe Leu Arg Phe
      130             135             140

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Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp  
 145 150 155 160  
 Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro  
 165 170 175  
 Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys  
 180 185 190  
 Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe  
 195 200 205  
 Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu  
 210 215 220  
 Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys  
 225 230 235 240  
 Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys  
 245 250 255  
 Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val  
 260 265 270  
 Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala  
 275 280 285  
 Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe  
 290 295 300  
 Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe  
 305 310 315 320  
 Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser  
 325 330 335  
 Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn  
 340 345 350  
 Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro  
 355 360 365  
 Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys  
 370 375 380  
 Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met  
 385 390 395 400  
 Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys  
 405 410 415  
 Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys  
 420 425 430  
 Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile  
 435 440 445  
 Thr

<210> 147  
 <211> 1580  
 <212> DNA  
 <213> Homo Sapiens

<400> 147  
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 ataaccggag cgctcccat ggaccacacg gagggcttgc ccgcggagga gccgcctgcg 120  
 catgctccat cgctgggaa atttggtgag cggcctccac ctaaacgact tactagggaa 180  
 gctatgcgaa attattttaaa agagcgaggg gatcaaacag tacttattct tcatgcaaaa 240  
 gttgcacaga agtcatatgg aaatgaaaaa aggtttttt gccacctcc ttgtgtatat 300  
 cttatgggca gcgatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa 360  
 caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420  
 cttaaacttg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac 480

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aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattgggt 540
gtgttcctca gcaagcggat aaaagtcatc tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcât tgcctcagga acaaagggtg ctctgtttta tcgactacga 660
tcccagacag ttagtaccag atacttgcât gtagaaggag gtaattttca tgccagttca 720
cagcagtggg gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa 780
ttcacagtcc gagatgtctâ catccattat ggacaaacat gcaaacttgt gtgctcagtt 840
actggcatgg cactcccaag attgataaât atgaaagtgt ataagcâac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat tttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
aaagaaccaa ataaagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat 1080
aaggcagagt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcaactccaaa tttacgagtg tggtttgggg atgtagaagc tgaaactatg 1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaagggt 1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tggtcgaaa tgatggaatc 1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccacg gccacattgc 1440
agtgtagcag gagcaatcct tccagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggatccta 1580

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&lt;210&gt; 148

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 148

```

Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
1      5      10      15
Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr
20     25     30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
35     40     45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
50     55     60
Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
65     70     75     80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
85     90     95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
100    105    110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
115    120    125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
130    135    140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
145    150    155    160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
165    170    175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
180    185    190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
195    200    205
Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu
210    215    220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

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225		230		235		240									
Tyr	Ile	His	Tyr	Gly	Gln	Thr	Cys	Lys	Leu	Val	Cys	Ser	Val	Thr	Gly
				245					250					255	
Met	Ala	Leu	Pro	Arg	Leu	Ile	Ile	Met	Lys	Val	Asp	Lys	His	Thr	Ala
			260					265					270		
Leu	Leu	Asp	Ala	Asp	Asp	Pro	Val	Ser	Gln	Leu	His	Lys	Cys	Ala	Phe
		275					280					285			
Tyr	Leu	Lys	Asp	Thr	Glu	Arg	Met	Tyr	Leu	Cys	Leu	Ser	Gln	Glu	Arg
	290					295					300				
Ile	Ile	Gln	Phe	Gln	Ala	Thr	Pro	Cys	Pro	Lys	Glu	Pro	Asn	Lys	Glu
305					310					315				320	
Met	Ile	Asn	Asp	Gly	Ala	Ser	Trp	Thr	Ile	Ile	Ser	Thr	Asp	Lys	Ala
			325					330					335		
Glu	Tyr	Thr	Phe	Tyr	Glu	Gly	Met	Gly	Pro	Val	Leu	Ala	Pro	Val	Thr
		340						345					350		
Pro	Val	Pro	Val	Val	Glu	Ser	Leu	Gln	Leu	Asn	Gly	Gly	Gly	Asp	Val
	355						360					365			
Ala	Met	Leu	Glu	Leu	Thr	Gly	Gln	Asn	Phe	Thr	Pro	Asn	Leu	Arg	Val
	370					375					380				
Trp	Phe	Gly	Asp	Val	Glu	Ala	Glu	Thr	Met	Tyr	Arg	Cys	Gly	Glu	Ser
385					390					395				400	
Met	Leu	Cys	Val	Val	Pro	Asp	Ile	Ser	Ala	Phe	Arg	Glu	Gly	Trp	Arg
			405					410					415		
Trp	Val	Arg	Gln	Pro	Val	Gln	Val	Pro	Val	Thr	Leu	Val	Arg	Asn	Asp
		420						425					430		
Gly	Ile	Ile	Tyr	Ser	Thr	Ser	Leu	Thr	Phe	Thr	Tyr	Thr	Pro	Glu	Pro
	435						440					445			
Gly	Pro	Arg	Pro	His	Cys	Ser	Val	Ala	Gly	Ala	Ile	Leu	Pro	Ala	Asn
	450						455				460				
Ser	Ser	Gln	Val	Pro	Pro	Asn	Glu	Ser	Asn	Thr	Asn	Ser	Glu	Gly	Ser
465					470					475				480	
Tyr	Thr	Asn	Ala	Ser	Thr	Asn	Ser	Thr	Ser	Val	Thr	Ser	Ser	Thr	Ala
			485					490					495		
Thr	Val	Val	Ser												
			500												

<210> 149  
 <211> 1248  
 <212> DNA  
 <213> Homo Sapiens

<400> 149	
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gccgccatgc gcgacaggac ccacgagctg agacaggggg atgacagctc ggacgaagag	120
gacaaggagc gggtcgcgct ggtggtgcac ccgggcacgg cacggctggg gagcccgac	180
gaggagttct tccacaaggt ccggacaatt cgtcagacta ttgtcaaact ggggaataaa	240
gtccaggagt tggagaaaca gcaggtcacc atcctggcca cgcccttcc cgaggagagc	300
atgaagcagg agctgcagaa cctgcgcgat gagatcaaac agctggggag ggagatccgc	360
ctgcagctga aggccataga gcccagaag gaggaagctg atgagaacta taactccgtc	420
aacacaagaa tgagaaaaac ccagcatggg gtcctgtccc agcaattcgt ggagctcatc	480
aacaagtgca attcaatgca gtccgaatac cgggagaaga acgtggagcg gattcggagg	540
cagctgaaga tcaccaatgc tggcatggtg tctgatgagg agttggatca gatgctggac	600
agtgggcaaa gcgaggtgtt tgtgtccaat atccttaagg acacgcaggt gactcgacag	660
gccttaaatg agatctcggc ccggcacagt gagatccagc agcttgaacg cagtattcgt	720
gagctgcacg acatattcac ttttctggct accgaagtgg agatgcaggg ggagatgatc	780

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aatcggattg agaagaacat cctgagctca gcggaactacg tggaacgtgg gcaggagcac      840
gtcaagacgg ccctggagaa ccagaagaag gtgaggaaga agaaagtctt gattgccatc      900
tgtgtgtcca tcaccgtcgt cctcctagca gtcacattg gcgtcacagt ggttggataa      960
tgtcgcacat tggtggcact aggagcacca ggaaccagg gcctggcctt ctctccagc      1020
agcctggggg gcaggcagag cctccagtcg gaccccttcc tcacacactg gccctatgc      1080
agaagggcag acagttcttc tggggttggc agctgtcat tcatgatggc ctctccttc      1140
aggcctcaat gcctggggga ggctgcact gtctgtattg gccgggacac acggttttgt      1200
aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt      1248

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&lt;210&gt; 150

&lt;211&gt; 297

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 150

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Met Arg Asp Arg Thr His Glu Leu Arg Gln Gly Asp Asp Ser Ser Asp
 1           5           10           15
Glu Glu Asp Lys Glu Arg Val Ala Leu Val Val His Pro Gly Thr Ala
 20           25           30
Arg Leu Gly Ser Pro Asp Glu Glu Phe Phe His Lys Val Arg Thr Ile
 35           40           45
Arg Gln Thr Ile Val Lys Leu Gly Asn Lys Val Gln Glu Leu Glu Lys
 50           55           60
Gln Gln Val Thr Ile Leu Ala Thr Pro Leu Pro Glu Glu Ser Met Lys
 65           70           75           80
Gln Glu Leu Gln Asn Leu Arg Asp Glu Ile Lys Gln Leu Gly Arg Glu
 85           90           95
Ile Arg Leu Gln Leu Lys Ala Ile Glu Pro Gln Lys Glu Glu Ala Asp
100          105          110
Glu Asn Tyr Asn Ser Val Asn Thr Arg Met Arg Lys Thr Gln His Gly
115          120          125
Val Leu Ser Gln Gln Phe Val Glu Leu Ile Asn Lys Cys Asn Ser Met
130          135          140
Gln Ser Glu Tyr Arg Glu Lys Asn Val Glu Arg Ile Arg Arg Gln Leu
145          150          155          160
Lys Ile Thr Asn Ala Gly Met Val Ser Asp Glu Glu Leu Asp Gln Met
165          170          175
Leu Asp Ser Gly Gln Ser Glu Val Phe Val Ser Asn Ile Leu Lys Asp
180          185          190
Thr Gln Val Thr Arg Gln Ala Leu Asn Glu Ile Ser Ala Arg His Ser
195          200          205
Glu Ile Gln Gln Leu Glu Arg Ser Ile Arg Glu Leu His Asp Ile Phe
210          215          220
Thr Phe Leu Ala Thr Glu Val Glu Met Gln Gly Glu Met Ile Asn Arg
225          230          235          240
Ile Glu Lys Asn Ile Leu Ser Ser Ala Asp Tyr Val Glu Arg Gly Gln
245          250          255
Glu His Val Lys Thr Ala Leu Glu Asn Gln Lys Lys Val Arg Lys Lys
260          265          270
Lys Val Leu Ile Ala Ile Cys Val Ser Ile Thr Val Val Leu Leu Ala
275          280          285
Val Ile Ile Gly Val Thr Val Val Gly
290          295

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&lt;210&gt; 151

&lt;211&gt; 1953

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 151

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acgcctgcc  ggagcaagcc  gaagagccag  cgggccggcg  cactccgact  ccgagcagtc      60
tctgtccttc  gacccgagcc  ccgcgccctt  tccgggaccc  ctgccccgcg  ggcagcgctg     120
ccaacctgcc  ggccatggag  accccgtccc  agcggcgcg  caccgcagc  ggggcgcagg     180
ccagctccac  tccgctgtcg  cccaccgcga  tcaccggct  gcaggagaag  gaggacctgc     240
aggagctcaa  tgatcgcttg  gcggtctaca  tcgaccgtgt  gcgctcgctg  gaaacggaga     300
acgcaggggct  gcgccttcgc  atcaccgagt  ctgaagaggt  ggtcagccgc  gagggtgccg     360
gcatcaaggc  cgcctacgag  gccgagctcg  gggatgcccg  caagaccctt  gactcagtag     420
ccaaggagcg  cgcgcgctg  cagctggagc  tgagcaaagt  gcgtgaggag  ttaaggagc     480
tgaaagcgcg  caataccaag  aaggagggtg  acctgatagc  tgctcaggct  cggctgaagg     540
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gcacgctgga  gggcgagctg  catgatctgc  ggggccagg  ggccaagctt  gaggcagccc     660
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agtctgctga  gaggaacagc  aacctgggtg  gggctgccc  cgaggagctg  cagcagtcgc    1020
gcacccgat  cgacagcctc  tctgccagc  tcagccagct  ccagaagcag  ctggcagcca    1080
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aggatggaga  tgacctgctc  catcaccacc  acgtgagtgg  tagccgccc  tgaggccgag    1860
cctgcactgg  ggccaccagc  caggcctggg  ggcagcctct  cccagcctc  cccgtgccaa    1920
aaatcttttc  attaaagaat  gttttggaac  ttt

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&lt;210&gt; 152

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 152

```

Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
 1             5             10            15
Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
      20            25            30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
      35            40            45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
      50            55            60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65             70             75             80

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Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala  
 85 90 95  
 Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu  
 100 105 110  
 Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile  
 115 120 125  
 Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys  
 130 135 140  
 Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly  
 145 150 155 160  
 Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu  
 165 170 175  
 Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp  
 180 185 190  
 Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys  
 195 200 205  
 Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr  
 210 215 220  
 Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg  
 225 230 235 240  
 Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val  
 245 250 255  
 Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp  
 260 265 270  
 Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala  
 275 280 285  
 His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala  
 290 295 300  
 Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu  
 305 310 315 320  
 Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg  
 325 330 335  
 Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met  
 340 345 350  
 Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala  
 355 360 365  
 Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
 370 375 380  
 Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly  
 385 390 395 400  
 Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr  
 405 410 415  
 Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln  
 420 425 430  
 His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu  
 435 440 445  
 Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met  
 450 455 460  
 Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr  
 465 470 475 480  
 Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr  
 485 490 495  
 Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu  
 500 505 510  
 Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515                      520                      525  
 Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val  
 530                      535                      540  
 Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp  
 545                      550                      555                      560  
 Leu Leu His His His His Val Ser Gly Ser Arg Arg  
                          565                      570

<210> 153  
 <211> 1610  
 <212> DNA  
 <213> Homo Sapiens

<400> 153  
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 cgggcctttg tgaatatgtg taagcaggat cggagcggtc tgtacaccga ggaaatgcgc 180  
 ttctgaggg agtgggtgga gagcataggt ggtaaagtac cacctgctac tcagaaagct 240  
 atatcagaag aaaataccaa ggaagaaaaa cctgatagta agaagtgga ggaagactta 300  
 aaggcagacg aaccatcaag tgaggaaagt gatctagaaa ttgataaaga aggtgtgatt 360  
 gaaccagaca ctgatgctcc tcaagaaatg ggagatgaaa atgcggagat aacggaggag 420  
 atgatggatc aggcataatga taaaaaagt gctgctattg aagccctaaa tgatggtgaa 480  
 ctccagaaag ccattgactt attcacagat gccatcaagc tgaatcctcg cttggccatt 540  
 ttgtatgcca agagggccag tgtcttcgct aaattacaga agccaaatgc tgccatccga 600  
 gactgtgaca gagccattga aataaatcct gattcagctc agccttaca gtggcggggg 660  
 aaagcacaca gacttctagg ccactgggaa gaagcagccc atgatcttgc ccttgctgtg 720  
 aaattggatt atgatgaaga tgctagtga atgctgaaag aagttcaacc tagggcacag 780  
 aaaattgcag aacatcggag aaagtatgag cgaaaacgtg aagagcgaga gatcaaagaa 840  
 agaatagaac gagttaagaa ggctcgagaa gagcatgaga gagcccagag ggaggaagaa 900  
 gccagacgac agtcaggagc tcagtatggc tcttttccag gtggccttcc tgggggaatg 960  
 cctggtaatt tccccggagg aatgcctgga atgggagggg gcatgcctgg aatggctgga 1020  
 atgcctggac tcaatgaaat tcttagtgat ccagaggttc ttgcagccat gcaggatcca 1080  
 gaagttatgg tggtcttcca ggatgtggct cagaacccag caaatatgtc aaaataccag 1140  
 agcaacccaa aggttatgaa tctcatcagt aaattgtcag ccaaatttgg aggtcaagcg 1200  
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 tttgaagata atccctaccc ctctccccc aatgcagctg aagcatttta cagtggtttg 1380  
 ccattagggg attcattcag ataattgttt cctactagga attacaaact ttaaactatt 1440  
 tttaaatctt caaaatattt aaaacaaatt taaagggcct gtttaattctt atatttttct 1500  
 ttactaatca ttttggattt ttttctttga attattggca gggaatatac ttatgtatgg 1560  
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<210> 154  
 <211> 369  
 <212> PRT  
 <213> Homo Sapiens

<400> 154  
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 1                      5                      10                      15  
 Lys Gln Asp Pro Ser Val Leu Tyr Thr Glu Glu Met Arg Phe Leu Arg  
 20                      25                      30  
 Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys  
 35                      40                      45  
 Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys

50	55	60
Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp		
65	70	75
Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro		80
	85	90
Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp		95
	100	105
Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly		110
	115	120
Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn		125
	130	135
Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys		140
145	150	155
Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu		160
	165	170
Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His		175
	180	185
Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala		190
	195	200
Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val		205
	210	215
Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg		220
225	230	235
Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys		240
	245	250
Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg		255
	260	265
Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly		270
	275	280
Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met		285
	290	295
Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro		300
305	310	315
Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln		320
	325	330
Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro		335
	340	345
Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln		350
	355	360
Ala		365

<210> 155  
 <211> 1323  
 <212> DNA  
 <213> Homo Sapiens

<400> 155

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cagaaaagat ggaaaaaagg acatgtgcac tctgccccaa agatgtcgaa tataatgtcc	180
tgtactttgc acaatcagag aatatagctg ctcatgagaa ttgtttgctg tattcttcag	240
gacttgtgga atgtgaggat caggatccac ttaatcctga tagaagtttt gatgtggaat	300
cagtaaagaa agaaatccag agaggaagga agttgaaatg caaattttgt cataaaagag	360
gagccaccgt gggatgtgat ttaaaaaact gtaacaagaa ttaccacttt ttctgtgcc	420



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agaaggacga cgcagttcca cagtctgatg gagttcgagg aatttataaa ctgctttgcc 480
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aaagaggaag gaagaaaccc ctctcaggca atcatgtaca gccacccgaa acaatgaaat 600
gtaatacatt cataagacaa gtgaaagaag agcatggcag acacacagat gcaactgtga 660
aagttccttt tcttaagaaa tgcaagggaa gcaggacttc ttaattactt acttgaagaa 720
atattagnca aagttcattc aattccagaa aaactcatgg atgagactta cttcagaatc 780
agactatgaa gaaatcgga gtgcactttt tgactgtaga ttgttcgaag acacatttgt 840
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gaaggaagag attgagctac ttcaggactt aaaacaaacc ttgtgctctt ttcaagaaaa 960
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tcctaagcca agagtcatgt caaattgcaa tcaggctcaa aaccagagac caggctgtga 1080
aatccacaca tctttagaac tagtcgtctc ctcttggcct cagcagctct tccctgttct 1140
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tcccagcacc tagtatgctc agtaaatggt tgtggaataa gtgcataaaa tgttcttaac 1260
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aaa 1323

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<210> 156  
 <211> 191  
 <212> PRT  
 <213> Homo Sapiens

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<400> 156
Met Glu Lys Arg Thr Cys Ala Leu Cys Pro Lys Asp Val Glu Tyr Asn
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Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
20 25 30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
35 40 45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
50 55 60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65 70 75 80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
85 90 95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
100 105 110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
115 120 125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
130 135 140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
145 150 155 160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
165 170 175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
180 185 190

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<210> 157  
 <211> 4065  
 <212> DNA  
 <213> Homo Sapiens

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<400> 157
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ttggattttc	ctgccttaag	aaaaaaca	aatattgaca	actttttaag	cagatataaa	180
gacacaataa	ataaaatcag	agattttacga	atgaaagctg	aagattatga	agtagtgaag	240
gtgattggta	gaggtgcatt	tggagaagtt	caattggtaa	ggcataaatc	caccaggaag	300
gtatatgcta	tgaagcttct	cagcaaattt	gaaatgataa	agagatctga	ttctgctttt	360
ttctgggaag	aaagggacat	catggctttt	gccaacagtc	cttgggttgt	tcagcttttt	420
tatgcattcc	aagatgatcg	ttatctctac	atggtgatgg	aatacatgcc	tgggtggagat	480
cttgtaaaact	taatgagcaa	ctatgatgtg	cctgaaaaat	gggcacgatt	ctatactgca	540
gaagtagttc	ttgcatttga	tgcaatccat	tccatgggtt	ttattcacag	agatgtgaag	600
cctgataaca	tgctgctgga	taaatctgga	catttgaagt	tagcagattt	tgggtacttgt	660
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gattctttgg	ttggaactta	cagtaaaatt	atgaaccata	aaaattcact	tacctttcct	900
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gaagtgaagt	tagggcgaaa	tgggtgtagaa	gaaatcaaac	gacatctctt	cttcaaaaat	1020
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cactcagaaa	aggaaaagaa	taatttagag	atagatttaa	actacaaact	taaatcatta	2040
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gagctaacag	agaaaatgaa	gaaggcagag	gaagaatata	aactggagaa	ggaggaggag	2940
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caggctgtta	acaaattggc	agaaataatg	aatcgaaaag	attttaaaat	tgatagaaag	3060
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ctcaaccaag	aaagagagaa	attcaaccag	atggtagtga	aacatcagaa	ggaactgaat	3180
gacatgcaag	cgcaattggg	agaagaatgt	gcacatagga	atgagcttca	gatgcagttg	3240
gccagcaaa	agagtgatat	tgagcaattg	cgtgctaaac	ttttggacct	ctcggattct	3300
acaagtgttg	ctagttttcc	tagtgctgat	gaaactgatg	gtaacctccc	agagtcagaa	3360

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caatccaatc catctatggg attggacata gataaactgt ttcacgtag acctgtaacc 3540
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gcaaataag gtgaatgtag aaaagatgta gagatggaac cagtacaaca agctgaaaaa 3660
actaatttcc aaaatcacaa aggccatgag tttattccta cactctacca ctttcctgcc 3720
aattgtgatg cctgtgccaa acctctctgg catgttttta agccaccccc tgccttagag 3780
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tctttccgga aagtgggtcaa aaatacatct ggaaaaacta gttaa 4065

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<210> 158  
 <211> 1354  
 <212> PRT  
 <213> Homo Sapiens

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<400> 158
Met Ser Thr Gly Asp Ser Phe Glu Thr Arg Phe Glu Lys Met Asp Asn
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Leu Leu Arg Asp Pro Lys Ser Glu Val Asn Ser Asp Cys Leu Leu Asp
 20          25          30
Gly Leu Asp Ala Leu Val Tyr Asp Leu Asp Phe Pro Ala Leu Arg Lys
 35          40          45
Asn Lys Asn Ile Asp Asn Phe Leu Ser Arg Tyr Lys Asp Thr Ile Asn
 50          55          60
Lys Ile Arg Asp Leu Arg Met Lys Ala Glu Asp Tyr Glu Val Val Lys
 65          70          75          80
Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
 85          90          95
Ser Thr Arg Lys Val Tyr Ala Met Lys Leu Leu Ser Lys Phe Glu Met
100          105          110
Ile Lys Arg Ser Asp Ser Ala Phe Phe Trp Glu Glu Arg Asp Ile Met
115          120          125
Ala Phe Ala Asn Ser Pro Trp Val Val Gln Leu Phe Tyr Ala Phe Gln
130          135          140
Asp Asp Arg Tyr Leu Tyr Met Val Met Glu Tyr Met Pro Gly Gly Asp
145          150          155          160
Leu Val Asn Leu Met Ser Asn Tyr Asp Val Pro Glu Lys Trp Ala Arg
165          170          175
Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met
180          185          190
Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
195          200          205
Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn
210          215          220
Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr
225          230          235          240
Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly
245          250          255
Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu
260          265          270
Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
275          280          285

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Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp  
 290 295 300  
 Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg  
 305 310 315 320  
 Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu  
 325 330 335  
 Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val  
 340 345 350  
 Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe  
 355 360 365  
 Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Thr Phe Pro Ile Pro  
 370 375 380  
 Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr  
 385 390 395 400  
 Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr  
 405 410 415  
 Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile  
 420 425 430  
 Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu  
 435 440 445  
 Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met  
 450 455 460  
 Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr  
 465 470 475 480  
 Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn  
 485 490 495  
 Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val  
 500 505 510  
 Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys  
 515 520 525  
 Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln  
 530 535 540  
 Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr  
 545 550 555 560  
 Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser  
 565 570 575  
 Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu  
 580 585 590  
 Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala  
 595 600 605  
 Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile  
 610 615 620  
 Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His  
 625 630 635 640  
 Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln  
 645 650 655  
 Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp  
 660 665 670  
 Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val  
 675 680 685  
 Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser  
 690 695 700  
 Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu  
 705 710 715 720  
 Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln

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Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val  
 1170 1175 1180  
 Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr  
 1185 1190 1195 1200  
 Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln  
 1205 1210 1215  
 Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile  
 1220 1225 1230  
 Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro  
 1235 1240 1245  
 Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys  
 1250 1255 1260  
 His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile  
 1265 1270 1275 1280  
 Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu  
 1285 1290 1295  
 Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu  
 1300 1305 1310  
 Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser  
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 1330 1335 1340  
 Val Val Lys Asn Thr Ser Gly Lys Thr Ser  
 1345 1350

<210> 159  
 <211> 683  
 <212> DNA  
 <213> Homo Sapiens

<400> 159  
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 gtaatgtggc acttgaatgc agtgagccaa gcacaagtgt atctgcttat gaccagttga 120  
 aggcaccggc atcccctggt gctggaaacc cacctgggac cccaaaggga aagagagagc 180  
 tgatgagcaa tggcccaggt tccattattg gtgctaaagc tgggaagaat tctggcaaaa 240  
 agaagggcct taacaatgaa ctgaacaacc ttccagtaat ctccaacatg acggctgcgt 300  
 tagacagttg ctcggcagca gacggcagtt tggctgctga gatgcctaaa ctggaagcag 360  
 aaggattaat tgacaagaaa aatttaggag ataaagaaaa gggcaaaaaa gctaacaact 420  
 gcaaaacgga caaaaacctc tctaaactga aaagtgcccg gcccaattgcc cctgccccag 480  
 cccccactcc cccgcagcta atcgctatac ccaactgcaac ctttacaacg accaccactg 540  
 ggacaatacc cggactgccc tccctcacia caactgttgt tcaggctaca ccaaagagtc 600  
 ctccgttaaa acccattcaa ccaaagccca caattatggg agagcccac accgtgaacc 660  
 cagctctggt gtcactcaaa gac 683

<210> 160  
 <211> 227  
 <212> PRT  
 <213> Homo Sapiens

<400> 160  
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 Glu Gly Leu Ser Asn Val Ala Leu Glu Cys Ser Glu Pro Ser Thr Ser  
 20 25 30  
 Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly Ala Gly

35 40 45  
 Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser Asn Gly  
 50 55 60  
 Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly Lys Lys  
 65 70 75 80  
 Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser Asn Met  
 85 90 95  
 Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu Ala Ala  
 100 105 110  
 Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys Asn Leu  
 115 120 125  
 Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr Asp Lys  
 130 135 140  
 Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala Pro Ala  
 145 150 155 160  
 Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe Thr Thr  
 165 170 175  
 Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr Thr Val  
 180 185 190  
 Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln Pro Lys  
 195 200 205  
 Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu Val Ser  
 210 215 220  
 Leu Lys Asp  
 225

<210> 161  
 <211> 662  
 <212> DNA  
 <213> Homo Sapiens

<400> 161  
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 acgctgagat gagtgaactg agtgtggcac agaaaccaga aaaacttttg gagcgctgca 120  
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 cagacatgc cttgaaatgg attcgacctc aaaccagcga atagcaccca gtcctgcctg 540  
 gcagaagatc atgcagtttg gaagttttca tgtctgatga aagatctcta cagaacttgt 600  
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 aa 662

<210> 162  
 <211> 173  
 <212> PRT  
 <213> Homo Sapiens

<400> 162  
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 Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro  
 20 25 30

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly  
 35 40 45  
 Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro  
 50 55 60  
 Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys  
 65 70 75 80  
 Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser  
 85 90 95  
 Arg Arg Ile Pro Val Leu Ser Pro Lys Pro Val Ala Pro Pro Ala Pro  
 100 105 110  
 Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met  
 115 120 125  
 Glu Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys  
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 Arg His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu  
 165 170

<210> 163  
 <211> 2912  
 <212> DNA  
 <213> Homo Sapiens

<400> 163  
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&lt;210&gt; 164

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 164

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Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
1      5      10      15
Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
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Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
35     40     45
Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu
50     55     60
Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
65     70     75     80
Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
85     90     95
Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
100    105    110
Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
115    120    125
Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val
130    135    140
Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
145    150    155    160
Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
165    170    175
Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
180    185    190
Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
195    200    205
Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
210    215    220
Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp

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225		230		235		240
Lys Glu Glu Glu	Lys Glu Lys Glu Glu	Lys Glu Ser Glu Asp Lys Pro				
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Glu Ile Glu Asp	Val Gly Ser Asp Glu Glu Glu Glu Lys Lys Asp Gly					
	260	265	270			
Asp Lys Lys Lys	Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln Glu					
	275	280	285			
Glu Leu Asn Lys Thr	Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp Ile					
	290	295	300			
Thr Asn Glu Glu Tyr	Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp Trp					
305	310	315	320			
Glu Asp His Leu	Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu					
	325	330	335			
Phe Arg Ala Leu	Phe Val Pro Arg Arg Ala Pro Phe Asp Leu Phe					
	340	345	350			
Glu Asn Arg Lys	Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg Val					
	355	360	365			
Phe Ile Met Asp	Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn Phe					
	370	375	380			
Ile Arg Gly Val	Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg					
385	390	395	400			
Glu Met Leu Gln	Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Leu					
	405	410	415			
Val Lys Lys Cys	Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys Glu					
	420	425	430			
Asn Tyr Lys Lys	Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu Gly					
	435	440	445			
Ile His Glu Asp	Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu Arg					
	450	455	460			
Tyr Tyr Thr Ser	Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp Tyr					
465	470	475	480			
Cys Thr Arg Met	Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr Gly					
	485	490	495			
Glu Thr Lys Asp	Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu Arg					
	500	505	510			
Lys His Gly Leu	Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu Tyr					
	515	520	525			
Cys Val Gln Gln	Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser Val					
	530	535	540			
Thr Lys Glu Gly	Leu Glu Leu Pro Glu Asp Glu Glu Lys Lys Lys					
545	550	555	560			
Gln Glu Glu Lys	Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met Lys					
	565	570	575			
Asp Ile Leu Glu	Lys Lys Val Glu Lys Val Val Val Ser Asn Arg Leu					
	580	585	590			
Val Thr Ser Pro	Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala					
	595	600	605			
Asn Met Glu Arg	Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr					
	610	615	620			
Met Gly Tyr Met	Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp His					
625	630	635	640			
Ser Ile Ile Glu	Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp					
	645	650	655			
Lys Ser Val Lys	Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu Leu					
	660	665	670			

Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile  
 675 680 685  
 Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr  
 690 695 700  
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 705 710 715 720  
 Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp  
 725 730

<210> 165  
 <211> 790  
 <212> DNA  
 <213> Homo. Sapiens

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 ttcaagggtcc tgtattaata ggaagttcac atggtggtgt caacattgaa gatgttctg 600  
 ctgagttctc tgaagcaata attaaagaac ctattgatat tgaagaaggc atcaaaaagg 660  
 aacaagctct tcagcttgca cagaagaatg ggatttcccc taatattgng ggaatcagca 720  
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 ggaaattaaa 790

<210> 166  
 <211> 259  
 <212> PRT  
 <213> Homo Sapiens

<400> 166  
 Asp Ser Glu Met Ala Ala Ser Met Phe Tyr Gly Arg Leu Val Ala Val  
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 Gln Val Leu Gly Ser Ser Gly Leu Phe Asn Asn His Gly Leu Gln Val  
 35 40 45  
 Gln Gln Gln Gln Gln Arg Asn Leu Ser Leu His Glu Tyr Met Ser Met  
 50 55 60  
 Glu Leu Leu Gln Glu Ala Gly Val Ser Val Pro Lys Gly Tyr Val Ala  
 65 70 75 80  
 Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys Leu Gly Ser Lys  
 85 90 95  
 Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly Arg Gly Lys Gly  
 100 105 110  
 Thr Phe Glu Ser Gly Leu Lys Gly Gly Val Lys Ile Val Phe Ser Pro  
 115 120 125  
 Glu Glu Ala Lys Ala Val Ser Ser Gln Met Ile Gly Lys Lys Leu Phe  
 130 135 140  
 Thr Lys Gln Thr Gly Glu Lys Gly Arg Ile Cys Asn Gln Val Leu Val

145		150		155		160									
Cys	Glu	Arg	Lys	Tyr	Pro	Arg	Arg	Glu	Tyr	Tyr	Phe	Ala	Ile	Thr	Met
		165		170		175									
Glu	Arg	Ser	Phe	Gln	Gly	Pro	Val	Leu	Ile	Gly	Ser	Ser	His	Gly	Gly
		180		185		190									
Val	Asn	Ile	Glu	Asp	Val	Ala	Ala	Glu	Ser	Pro	Glu	Ala	Ile	Ile	Lys
		195		200		205									
Glu	Pro	Ile	Asp	Ile	Glu	Glu	Gly	Ile	Lys	Lys	Glu	Gln	Ala	Leu	Gln
		210		215		220									
Leu	Ala	Gln	Lys	Asn	Gly	Ile	Ser	Pro	Asn	Ile	Gly	Ile	Ser	Ser	Arg
		225		230		235									
Lys	Thr	Trp	Ser	Ser	Phe	Thr	Phe	Leu	Lys	Tyr	Asp	Ala	Thr	Leu	Asp
		245		250		255									
Arg	Lys	Leu													

<210> 167  
 <211> 5307  
 <212> DNA  
 <213> Homo Sapiens

<400> 167

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gccattttac	caaaataaag	atatcaccaa	ggaagaatat	aaagaaattg	tacggaaagc	4500
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cccacaaaat	tcaagggaaa	gtaaagggtt	taaaggaatg	tgcattctta	ctaggactgt	4920
gttatagtgt	ggatactgga	aatgtatag	ctttttgatt	agggcaatgg	agtgcataaa	4980
ttagaaactt	ctaagtgcac	tggttttcaa	agagatatat	ataatgcatt	tattctgtca	5040
ggttaaaata	taaagtatga	tctttatgat	ttttccctc	taattataga	aagttaaata	5100
atgtattacc	atgaaaaatg	tttctaatat	taaatagaac	atatcagttg	caaagttcct	5160
aatgtgtatt	tttaaagcac	atatctgaat	aaattgccta	gatagaaaaa	aaattatcac	5220
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5307

&lt;210&gt; 168

&lt;211&gt; 1148

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 168

Met Thr Thr Pro Thr Arg Arg Ser Thr Arg Asn Thr Arg Ala Glu Thr  
 1 5 10 15  
 Ala Ser Gln Ser Gln Arg Ser Pro Ile Ser Asp Asn Ser Gly Cys Asp  
 20 25 30  
 Ala Pro Gly Asn Ser Asn Pro Ser Leu Ser Val Pro Ser Ala Glu  
 35 40 45  
 Ser Glu Lys Gln Thr Arg Gln Ala Pro Lys Arg Lys Ser Val Arg Arg  
 50 55 60  
 Gly Arg Lys Pro Pro Leu Leu Lys Lys Lys Leu Arg Ser Ser Val Ala  
 65 70 75 80  
 Ala Pro Glu Lys Ser Ser Ser Asn Asp Ser Val Asp Glu Glu Thr Ala  
 85 90 95  
 Glu Ser Asp Thr Ser Pro Val Leu Glu Lys Glu His Gln Pro Asp Val  
 100 105 110  
 Asp Ser Ser Asn Ile Cys Thr Val Gln Thr His Val Glu Asn Gln Ser  
 115 120 125  
 Ala Asn Cys Leu Lys Ser Cys Asn Glu Gln Ile Glu Glu Ser Glu Lys  
 130 135 140  
 His Thr Ala Asn Tyr Asp Thr Glu Glu Arg Val Gly Ser Ser Ser Ser  
 145 150 155 160  
 Glu Ser Cys Ala Gln Asp Leu Pro Val Leu Val Gly Glu Glu Gly Glu  
 165 170 175  
 Val Lys Lys Leu Glu Asn Thr Gly Ile Glu Ala Asn Val Leu Cys Leu  
 180 185 190  
 Glu Ser Glu Ile Ser Glu Asn Ile Leu Glu Lys Gly Gly Asp Pro Leu  
 195 200 205  
 Glu Lys Gln Asp Gln Ile Ser Gly Leu Ser Gln Ser Glu Val Lys Thr  
 210 215 220  
 Asp Val Cys Thr Val His Leu Pro Asn Asp Phe Pro Thr Cys Leu Thr  
 225 230 235 240  
 Ser Glu Ser Lys Val Tyr Gln Pro Val Ser Cys Pro Leu Ser Asp Leu  
 245 250 255  
 Ser Glu Asn Val Glu Ser Val Val Asn Glu Glu Lys Ile Thr Glu Ser  
 260 265 270  
 Ser Leu Val Glu Ile Thr Glu His Lys Asp Phe Thr Leu Lys Thr Glu  
 275 280 285  
 Glu Leu Ile Glu Ser Pro Lys Leu Glu Ser Ser Glu Gly Glu Ile Ile  
 290 295 300  
 Gln Thr Val Asp Arg Gln Ser Val Lys Ser Pro Glu Val Gln Leu Leu  
 305 310 315 320  
 Gly His Val Glu Thr Glu Asp Val Glu Ile Ile Ala Thr Cys Asp Thr  
 325 330 335  
 Phe Gly Asn Glu Asp Phe Asn Asn Ile Gln Asp Ser Glu Asn Asn Leu  
 340 345 350  
 Leu Lys Asn Asn Leu Leu Asn Thr Lys Leu Glu Lys Ser Leu Glu Glu

355	360	365
Lys Asn Glu Ser Leu Thr Glu His Pro Arg Ser Thr Glu Leu Pro Lys		
370	375	380
Thr His Ile Glu Gln Ile Gln Lys His Phe Ser Glu Asp Asn Asn Glu		
385	390	395
Met Ile Pro Met Glu Cys Asp Ser Phe Cys Ser Asp Gln Asn Glu Ser		400
405	410	415
Glu Val Glu Pro Ser Val Asn Ala Asp Leu Lys Gln Met Asn Glu Asn		
420	425	430
Ser Val Thr His Cys Ser Glu Asn Asn Met Pro Ser Ser Asp Leu Ala		
435	440	445
Asp Glu Lys Val Glu Thr Val Ser Gln Pro Ser Glu Ser Pro Lys Asp		
450	455	460
Thr Ile Asp Lys Thr Lys Lys Pro Arg Thr Arg Ser Arg Phe His		
465	470	475
Ser Pro Ser Thr Thr Trp Ser Pro Asn Lys Asp Thr Pro Gln Glu Lys		480
485	490	495
Lys Arg Pro Gln Ser Pro Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser		
500	505	510
Arg Lys Ser Gln Ser Pro Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg		
515	520	525
Lys Lys Ser Arg Ser Gln Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg		
530	535	540
Arg Gln Ser Gln Ser Arg Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser		
545	550	555
Arg Arg Ser Glu Ser Leu Ser Pro Arg Arg Glu Thr Ser Arg Glu Asn		
565	570	575
Lys Arg Ser Gln Pro Arg Val Lys Asp Ser Ser Pro Gly Glu Lys Ser		
580	585	590
Arg Ser Gln Ser Arg Glu Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg		
595	600	605
Glu Arg Glu Arg Arg Thr Arg Lys Trp Ser Arg Ser Arg Ser His Ser		
610	615	620
Arg Ser Pro Ser Arg Cys Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly		
625	630	635
Arg Ile Asp Arg Asp Ser Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala		
645	650	655
Asn Asp Gly Trp Arg Cys Pro Arg Gly Asn Asp Arg Tyr Arg Lys Asn		
660	665	670
Asp Pro Glu Lys Gln Asn Glu Asn Thr Arg Lys Glu Lys Asn Asp Ile		
675	680	685
His Leu Asp Ala Asp Asp Pro Asn Ser Ala Asp Lys His Arg Asn Asp		
690	695	700
Cys Pro Asn Trp Ile Thr Glu Lys Ile Asn Ser Gly Pro Asp Pro Arg		
705	710	715
Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu Glu Asn Arg		
725	730	735
Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly Ser Gly Trp		
740	745	750
Val Ser Asn Arg Gly Arg Gly Arg Gly Asn Arg Gly Arg Gly Thr Tyr		
755	760	765
Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg Trp Gln Asn		
770	775	780
Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser Glu Ser Phe		
785	790	795
		800

Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu Gln Glu Phe  
 805 810 815  
 Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser Ala Ser Ser  
 820 825 830  
 Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn Tyr Tyr Ser  
 835 840 845  
 Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp Met Lys Gln  
 850 855 860  
 Glu Glu Glu Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp Gln Thr Asn  
 865 870 875 880  
 Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met Gln Pro Gln  
 885 890 895  
 Met Asn Val Met Gln Gln Gln Met Asn Ala Gln His Gln Pro Met Asn  
 900 905 910  
 Ile Phe Pro Tyr Pro Val Gly Val His Ala Pro Leu Met Asn Ile Gln  
 915 920 925  
 Arg Asn Pro Phe Asn Ile His Pro Gln Leu Pro Leu His Leu His Thr  
 930 935 940  
 Gly Val Pro Leu Met Gln Val Ala Thr Pro Thr Ser Val Ser Gln Gly  
 945 950 955 960  
 Leu Pro Pro Pro Pro Pro Pro Pro Pro Ser Gln Gln Val Asn Tyr  
 965 970 975  
 Ile Ala Ser Gln Pro Asp Gly Lys Gln Leu Gln Gly Ile Pro Ser Ser  
 980 985 990  
 Ser His Val Ser Asn Asn Met Ser Thr Pro Val Leu Pro Ala Pro Thr  
 995 1000 1005  
 Ala Ala Pro Gly Asn Thr Gly Met Val Gln Gly Pro Ser Ser Gly Asn  
 1010 1015 1020  
 Thr Ser Ser Ser Ser His Ser Lys Ala Ser Asn Ala Ala Val Lys Leu  
 1025 1030 1035 104  
 Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp Ser Ser  
 1045 1050 1055  
 Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln Glu Val  
 1060 1065 1070  
 Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu  
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 Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Asp Lys Val Cys His Ser  
 1090 1095 1100  
 Lys Ser Gly Glu Val Asn Ser Thr Lys Val Ala Asn Leu Val Lys Ala  
 1105 1110 1115 112  
 Tyr Val Asp Lys Tyr Lys Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr  
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 1140 1145

&lt;210&gt; 169

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 169

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 gaagtgtctac caaaacacgc aatgactgtc ctaaaagtgc gttctgggat acacctgtaa 180  
 acttggtatca agttccctcc cctctcctca aaatatatcg acttgtgtctg aaagaaatca 240



cgaccgatgc	tcacaattct	gacctcgtaa	ttatataggg	ggtaggtttg	gtttctgcgt	300
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gcaaacaagg	gacagggcct	caaagtgtgc	ggtagggagc	caggaccccg	ccagtggcgt	420
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aagggtggc	taaggaggc	cggggcggag	gaagccaagc	tctgcaggcc	ctgacaaagt	540
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&lt;210&gt; 170

&lt;211&gt; 3344

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 170

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caggcatgaa	ccagtttaa	cccattttcc	tgaacacaat	tgacccatct	caccccatgg	300
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gtggctcttg	cagtggatc	cactacgacc	ggattgggtg	tcgggacgcc	gcacatcttg	720
tcaaccagga	cgacccta	gtgctggaga	tctggaacct	tgtgttcac	cagtataaca	780
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ctgcagtcac cccccagtgg cagaaggatg aattgcggga gactctcaaa tccctaaaga 2580
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<210> 171  
 <211> 1004  
 <212> PRT  
 <213> Homo Sapiens

<400> 171

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Tyr Ser Cys Ala Ser Ala Gly Ile Gly Ala Ala Gly Pro Trp Arg Gly
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Thr Leu Arg Glu Leu Gly Thr Ala Thr Leu Gly Glu Phe Phe Gly
20        25        30
Val Thr Phe Lys Met Asp Ser Thr Leu Thr Ala Ser Glu Ile Arg Gln
35        40        45
Arg Phe Ile Asp Phe Phe Lys Arg Asn Glu His Thr Tyr Val His Ser
50        55        60
Ser Ala Thr Ile Pro Leu Asp Asp Pro Thr Leu Leu Phe Ala Asn Ala
65        70        75        80
Gly Met Asn Gln Phe Lys Pro Ile Phe Leu Asn Thr Ile Asp Pro Ser
85        90        95
His Pro Met Ala Lys Leu Ser Arg Ala Ala Asn Thr Gln Lys Cys Ile
100       105       110
Arg Ala Gly Gly Lys Gln Asn Asp Leu Asp Asp Val Gly Lys Asp Val
115       120       125
Tyr His His Thr Phe Phe Glu Met Leu Gly Ser Trp Ser Phe Gly Asp
130       135       140
Tyr Phe Lys Glu Leu Ala Cys Lys Met Ala Leu Glu Leu Leu Thr Gln
145       150       155       160
Glu Phe Gly Ile Pro Ile Glu Arg Leu Tyr Val Thr Tyr Phe Gly Gly
165       170       175
Asp Glu Ala Ala Gly Leu Glu Ala Asp Leu Glu Cys Lys Gln Ile Trp
180       185       190
Gln Asn Leu Gly Leu Asp Asp Thr Lys Ile Leu Pro Gly Asn Met Lys
195       200       205
Asp Asn Phe Trp Glu Met Gly Asp Thr Gly Pro Cys Gly Pro Cys Ser
210       215       220
Glu Ile His Tyr Asp Arg Ile Gly Gly Arg Asp Ala Ala His Leu Val
225       230       235       240
Asn Gln Asp Asp Pro Asn Val Leu Glu Ile Trp Asn Leu Val Phe Ile
245       250       255
Gln Tyr Asn Arg Glu Ala Asp Gly Ile Leu Lys Pro Leu Pro Lys Lys
260       265       270

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Ser Ile Asp Thr Gly Met Gly Leu Glu Arg Leu Val Ser Val Leu Gln  
 275 280 285  
 Asn Lys Met Ser Asn Tyr Asp Thr Asp Leu Phe Val Pro Tyr Phe Glu  
 290 295 300  
 Ala Ile Gln Lys Gly Thr Gly Ala Arg Pro Tyr Thr Gly Lys Val Gly  
 305 310 315 320  
 Ala Glu Asp Ala Asp Gly Ile Asp Met Ala Tyr Arg Val Leu Ala Asp  
 325 330 335  
 His Ala Arg Thr Ile Thr Val Ala Leu Ala Asp Gly Gly Arg Pro Asp  
 340 345 350  
 Asn Thr Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Val  
 355 360 365  
 Arg Tyr Ala His Glu Lys Leu Asn Ala Ser Arg Gly Phe Phe Ala Thr  
 370 375 380  
 Leu Val Asp Val Val Val Gln Ser Leu Gly Asp Ala Phe Pro Glu Leu  
 385 390 395 400  
 Lys Lys Asp Pro Asp Met Val Lys Asp Ile Ile Asn Glu Glu Glu Val  
 405 410 415  
 Gln Phe Leu Lys Thr Leu Ser Arg Gly Arg Arg Ile Leu Asp Arg Lys  
 420 425 430  
 Ile Gln Ser Leu Gly Asp Ser Lys Thr Ile Pro Gly Asp Thr Ala Trp  
 435 440 445  
 Leu Leu Tyr Asp Thr Tyr Gly Phe Pro Val Asp Leu Thr Gly Leu Ile  
 450 455 460  
 Ala Glu Glu Lys Gly Leu Val Val Asp Met Asp Gly Phe Glu Glu Glu  
 465 470 475 480  
 Arg Lys Leu Ala Gln Leu Lys Ser Gln Gly Lys Gly Ala Gly Gly Glu  
 485 490 495  
 Asp Leu Ile Met Leu Asp Ile Tyr Ala Ile Glu Glu Leu Arg Ala Arg  
 500 505 510  
 Gly Leu Glu Val Thr Asp Asp Ser Pro Lys Tyr Asn Tyr His Leu Asp  
 515 520 525  
 Ser Ser Gly Ser Tyr Val Phe Glu Asn Thr Val Ala Thr Val Met Ala  
 530 535 540  
 Leu Arg Arg Glu Lys Met Phe Val Glu Glu Val Ser Thr Gly Gln Glu  
 545 550 555 560  
 Cys Gly Val Val Leu Asp Lys Thr Cys Phe Tyr Ala Glu Gln Gly Gly  
 565 570 575  
 Gln Ile Tyr Asp Glu Gly Tyr Leu Val Lys Val Asp Asp Ser Ser Glu  
 580 585 590  
 Asp Lys Thr Glu Phe Thr Val Lys Asn Ala Gln Val Arg Gly Gly Tyr  
 595 600 605  
 Val Leu His Ile Gly Thr Ile Tyr Gly Asp Leu Lys Val Gly Asp Gln  
 610 615 620  
 Val Trp Leu Phe Ile Asp Glu Pro Arg Arg Arg Pro Ile Met Ser Asn  
 625 630 635 640  
 His Thr Ala Thr His Ile Leu Asn Phe Ala Leu Arg Ser Val Leu Gly  
 645 650 655  
 Glu Ala Asp Gln Lys Gly Ser Leu Val Ala Pro Asp Arg Leu Arg Phe  
 660 665 670  
 Asp Phe Thr Ala Lys Gly Ala Met Ser Thr Gln Gln Ile Lys Lys Ala  
 675 680 685  
 Glu Glu Ile Ala Asn Glu Met Ile Glu Ala Ala Lys Ala Val Tyr Thr  
 690 695 700  
 Gln Asp Cys Pro Leu Ala Ala Ala Lys Ala Ile Gln Gly Leu Arg Ala

705		710		715		720
Val Phe Asp Glu Thr Tyr Pro Asp Pro Val Arg Val Val Ser Ile Gly						
	725		730		735	
Val Pro Val Ser Glu Leu Leu Asp Asp Pro Ser Gly Pro Ala Gly Ser						
	740		745		750	
Leu Thr Ser Val Glu Phe Cys Gly Gly Thr His Leu Arg Asn Ser Ser						
	755		760		765	
His Ala Gly Ala Phe Val Ile Val Thr Glu Glu Ala Ile Ala Lys Gly						
	770		775		780	
Ile Arg Arg Ile Val Ala Val Thr Gly Ala Glu Ala Gln Lys Ala Leu						
785		790		795		800
Arg Lys Ala Glu Ser Leu Lys Lys Cys Leu Ser Val Met Glu Ala Lys						
	805		810		815	
Val Lys Ala Gln Thr Ala Pro Asn Lys Asp Val Gln Arg Glu Ile Ala						
	820		825		830	
Asp Leu Gly Glu Ala Leu Ala Thr Ala Val Ile Pro Gln Trp Gln Lys						
	835		840		845	
Asp Glu Leu Arg Glu Thr Leu Lys Ser Leu Lys Lys Val Met Asp Asp						
	850		855		860	
Leu Asp Arg Ala Ser Lys Ala Asp Val Gln Lys Arg Val Leu Glu Lys						
865		870		875		880
Thr Lys Gln Phe Ile Asp Ser Asn Pro Asn Gln Pro Leu Val Ile Leu						
	885		890		895	
Glu Met Glu Ser Gly Ala Ser Ala Lys Ala Leu Asn Glu Ala Leu Lys						
	900		905		910	
Leu Phe Lys Met His Ser Pro Gln Thr Ser Ala Met Leu Phe Thr Val						
	915		920		925	
Asp Asn Glu Ala Gly Lys Ile Thr Cys Leu Cys Gln Val Pro Gln Asn						
	930		935		940	
Ala Ala Asn Arg Gly Leu Lys Ala Ser Glu Trp Val Gln Gln Val Ser						
945		950		955		960
Gly Leu Met Asp Gly Lys Gly Gly Gly Lys Asp Val Ser Ala Gln Ala						
	965		970		975	
Thr Gly Lys Asn Val Gly Cys Leu Gln Glu Ala Leu Gln Leu Ala Thr						
	980		985		990	
Ser Phe Ala Gln Leu Arg Leu Gly Asp Val Lys Asn						
	995		1000			

<210> 172  
 <211> 659  
 <212> DNA  
 <213> Homo Sapiens

<400> 172	
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<210> 173  
 <211> 192  
 <212> PRT  
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<400> 173  
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 Gln Leu Leu Ile Gly Gly Gly Leu Glu Ser Gly Gly Gln Gly Gly Ala  
 20 25 30  
 Glu Gln Pro Arg Arg Arg Arg Pro Asn Gln Pro Ser Arg Ile Leu Thr  
 35 40 45  
 Leu Lys Pro Ser Ile Phe His Leu Phe Ile Asn Met Glu Asn Ser Asp  
 50 55 60  
 Ser Asn Asp Lys Gly Ser Gly Asp Gln Ser Ala Ala Gln Arg Arg Ser  
 65 70 75 80  
 Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe Tyr Gln Phe Val Asn  
 85 90 95  
 Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg Asp Asn Asn Leu Leu  
 100 105 110  
 Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu Leu Arg Arg Leu Gln  
 115 120 125  
 Gln Ile Lys Glu Gly Pro Pro Pro Gln Asn Ser Asp Glu Asn Arg Gly  
 130 135 140  
 Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp Ser Ile Ile Asp Trp  
 145 150 155 160  
 Leu Asn Ser Val Arg Gln Thr Gly Asn Thr Thr Arg Ser Gly Gln Arg  
 165 170 175  
 Gly Asn Gln Ser Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Ser Gly  
 180 185 190

<210> 174  
 <211> 610  
 <212> DNA  
 <213> Homo Sapiens

<400> 174  
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 caaccccaaa tctgccacag agcagtcagg aactgggtatc cgatcagaga gtgagacaga 180  
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 ccaggggggag gactacggca aaggtgtcat cttctacctc agggacaaag tggctcgtggg 300  
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 cccacagtg gaattggcaa acccactgca gccctgaga ggaggtcgaa tgggtaaagg 480  
 agcatttttt tattcagcag actttctctg tgtatgagtg tgaatgatca agtcctttgt 540  
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 cttctaaaaa 610

<210> 175  
 <211> 138  
 <212> PRT  
 <213> Homo Sapiens

<400> 175

Tyr Trp His Gln Ser Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly  
 1 5 10 15  
 Tyr Glu Ala Ile Gly Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val  
 20 25 30  
 Rhe Ala Lys Ala Thr Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln  
 35 40 45  
 Ser Gly Thr Gly Ile Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser  
 50 55 60  
 Glu Ile Thr Ile Pro Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val  
 65 70 75 80  
 Gln Gly Glu Asp Tyr Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys  
 85 90 95  
 Val Val Val Gly Ile Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile  
 100 105 110  
 Ala Arg Lys Ile Ile Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu  
 115 120 125  
 Val Ala Lys Leu Phe Asn Ile His Glu Asp  
 130 135

<210> 176  
 <211> 805  
 <212> DNA  
 <213> Homo Sapiens

<400> 176  
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 gtccgcgcca tggccatcta caagcagtca cagcacatga cggagggtgt gaggcgctgc 180  
 cccaccatg agcgtgctc agatagcgat ggtctggccc ctctcagca tcttatccga 240  
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 ctggaagact ccagtggtaa tctactggga cggaacagct ttgagggtgc tgtttgtgcc 480  
 tgctctggga gagaccggcg cacagaggaa gagaatctcc gcaagaaagg ggagcctcac 540  
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 gaaagttcca aaaaangggg ccagt 805

<210> 177  
 <211> 626  
 <212> DNA  
 <213> Homo Sapiens

<400> 177  
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 caggtttgca ggcaggcgt catgagtgc ggtggaaggc tccgagggcg tgggcagggg 180  
 ctggggcggg gccacacact tgtggagcta gaaatantgg ggcaggctct tctctatcac 240  
 caggggctcc tccatgggtc cgtagcgctt caccacgcag ccgttcttgt cgatgaggaa 300  
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 cctgtccgct gccatcttg gccacggctg tggccagggg aaactggctc cctaccccc 420  
 acagccccct tacctttggg gaagttccac ttgatggcac tggaaaanaa gcacatggac 480  
 gtgagcgtcc ccaggcagcc cccacagtc cccaaagctt gtcctgtctc caaggaggcc 540

anaaagggttg tnagcttccc ccggtncctc cacangccac agtgccccca aanccccccc 600  
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<210> 178

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 178

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 agggcgtgct ggagaagcgc agcgacgggt tgttgagct ctggaagaaa aagtgttgca 180  
 tcctcaccga ggaagggtgt ctgcttatcc cggccaagca gctgcaaac cagcagcagc 240  
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 tggatgatgg agagggcaag gagatcgact ttcgggtgcc gcaagaccag ggctggaacg 480  
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 agccgcagct ccaagcccca acccagcct tcagcctcaa gccngcaacc ccaagcccca 660  
 attcacaac ccaagccct caagcccca ccaagccc tcangcccca ngcaagntcc 720  
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 acccaanaac nct 793

<210> 179

<211> 786

<212> DNA

<213> Homo Sapiens

<400> 179

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 ctccaagatt aggaattact acggattagg tttttgaaaa taaagtctcc tttttggaaa 180  
 atggtctaca ttcagaaatg tcttagaaca agcattttaa aaaaactaat aaataatcat 240  
 aatcaaaat acattaaaat aaaattacag tacatcatcg ctccatagaaa attcaccata 300  
 caagacgatc ctttcaaagg ttcataaata aaagtcttct tgactcgaaa tcggttctctg 360  
 catcgtgatg aaaagtatgc agaaaactaa gaagaatcgc aagttttcag taggggtgatg 420  
 tccaaactac ttgatctggt gcggggcgga gagactgttt tgcttttgat ccaagtgaag 480  
 acaatagaaa tgtgctcgtc ccacttcctc aagtcctcaa aacctgtct tgcccgggag 540  
 ctgccccttt cangcagagt tgggaggtgc tgcgganaaa ccggtgccc tgccggtgcc 600  
 aatgcggctg tgggtgtggg tgcngtatct ggtgccggat gcnggtgcc ggtnaagggt 660  
 tggggtgcca antnaaggat gaaaatgtgg atnttngnat nttgattccg gatacggggt 720  
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<210> 180

<211> 791

<212> DNA

<213> Homo Sapiens

<400> 180

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 cctcatggc ctcttctccg acttctatct gtgtgtgtgg gcaggtgcca gctgggggtg 180  
 gagttctgca gtgtgacctg tgtcaggact ggttccatgg gcagtgtgtg tcagtgcacc 240

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aaggcagtgg	caacaatatt	tcnaangtcc	aagggctgct	ggagaatgga	gacantgttg	660
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cctggaggga	g					791

&lt;210&gt; 181

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 181

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ggagaattgt	ancaaaggca	ttaaagaagg	gacaagcaag	ctgaagagcc	tgaatccttg	660
gggttgtaag	ccnatttttg	gnttcctttc	aagaaaaggg	ctgttggncc	gtggaanggg	720
tcanggaaca	ntatttcacg	ggtcngc				747

&lt;210&gt; 182

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 182

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acctaggaat	ccaacttaca	aaggatgtga	aggacctctt	caaggagaac	tacaaaccac	120
tgctcaatga	aataaaagag	gatacaaaaca	aatggaagaa	cattccatgc	tcatgggtag	180
gaagaatcaa	tatcgtgaaa	atggccatac	tgcccaaggt	aatgtataga	ttcaatgcc	240
tcccatcaa	gctaccaatg	actttcttca	cagaatttga	aaaaactact	caaaagttca	300
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aggattccct	atttaataaa	tgggtgctggg	aaaactggct	agccatatgt	agaaagctga	600
aactggatct	cttctttata	ccttatacaa	aaattaattg	aagatggntt	aaaggactta	660
aacgttagac	ctaaaaccat	aaaaacccta	gaagaaaaac	ctaggcatta	ccattcangg	720
acataggctt	gggcaaggac	ttcctgtcta	aaacaccaan	agcaatggga	ncaaaagcca	780
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agagngaaca	ggaacntcaa	antgggagaa	atthtgaacc	taccatcnga	naaggcta	900
nccagaatc						909

&lt;210&gt; 183



&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 183

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gtatacatgt	gccatgctgg	tgtgctgcac	ccattaactc	gttatttagc	attaggtata	120
tctcctaagt	ctatccctcc	cgcctcccc	cacccacaa	cagtcgccag	agtgtgatgt	180
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tcccggaactt	tttaanggat	tgncaatcc	aaccggngt	caaaagg		708

&lt;210&gt; 184

&lt;211&gt; 855

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 184

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&lt;210&gt; 185

&lt;211&gt; 865

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 185

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&lt;210&gt; 186

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 186

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aattttctga	agcaagctga	gaggcaggca	gaaagatttg	atgccaaaaa	aaaaaaaatc	240
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&lt;210&gt; 187

&lt;211&gt; 946

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 187

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&lt;210&gt; 188

&lt;211&gt; 802

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 188

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&lt;210&gt; 189

&lt;211&gt; 807

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 189

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&lt;210&gt; 190

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 190

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 <212> DNA  
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 ttctggangg ccatttgagg aaaccaaaac ctggggctcn acaaccctgt ccangcctgt 720  
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 tcagaa 786

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 <213> Homo Sapiens

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gcaagtttca	agattgggaa	gtta				744

&lt;210&gt; 194

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 194

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&lt;210&gt; 195

&lt;211&gt; 771

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 195

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ccaagaaaga	ancanaaaag	aaagcaaaag	cagaagctaa	acggaaggag	caagaagcta	180
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&lt;210&gt; 196

&lt;211&gt; 561

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 196

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antgtngnat	naccgncngn	c				561

&lt;210&gt; 197

&lt;211&gt; 691

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 197

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&lt;210&gt; 198

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 198

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&lt;210&gt; 199

&lt;211&gt; 811

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 199

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&lt;210&gt; 200

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 200

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&lt;210&gt; 201

&lt;211&gt; 717

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 201

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&lt;210&gt; 202

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 202

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&lt;210&gt; 203

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 203

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&lt;210&gt; 204

&lt;211&gt; 738

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 204

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&lt;210&gt; 205

&lt;211&gt; 818

&lt;212&gt; DNA



## &lt;213&gt; Homo Sapiens

&lt;400&gt; 205

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&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 206

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&lt;210&gt; 207

&lt;211&gt; 910

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 207

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aaact						965

<210> 210  
 <211> 867

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 210

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aaccngttct	tggggcaaaa	tttttaa				867

&lt;210&gt; 211

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 211

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&lt;210&gt; 212

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 212

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&lt;210&gt; 213

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 213

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 214

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 215

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&lt;211&gt; 824

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 216

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&lt;211&gt; 749

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 217

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<210> 218  
 <211> 600  
 <212> DNA  
 <213> Homo Sapiens

<400> 218

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<210> 219  
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 <212> DNA  
 <213> Homo Sapiens

<400> 219

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 <212> DNA  
 <213> Homo Sapiens

<400> 220

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&lt;210&gt; 221

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 221

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&lt;210&gt; 222

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 222

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&lt;210&gt; 223

&lt;211&gt; 747

&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 223

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## &lt;210&gt; 224

## &lt;211&gt; 618

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 224

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aaggcanccc	antcccag					618

## &lt;210&gt; 225

## &lt;211&gt; 765

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 225

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 <212> DNA  
 <213> Homo Sapiens

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 <211> 687  
 <212> DNA  
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 <212> DNA  
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&lt;210&gt; 229

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 229

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&lt;210&gt; 230

&lt;211&gt; 842

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 230

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ga						842

&lt;210&gt; 231

&lt;211&gt; 781

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 231

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c						781

&lt;210&gt; 232

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 232

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&lt;210&gt; 233

&lt;211&gt; 879

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 233

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&lt;210&gt; 234

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 234

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&lt;210&gt; 235

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 235

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&lt;210&gt; 236

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 236

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 <213> Homo Sapiens

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<210> 238  
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<400> 238  
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 tctgaaaaat ataagtacaa aagctaagta aacaatgagg tactgccatt tgggattttt 180  
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 tgtcactcct tccttcaa 678

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 <213> Homo Sapiens

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 atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat 180  
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&lt;210&gt; 240

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 240

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&lt;210&gt; 241

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 241

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 aacagattct ggggagtttt catcagttgg agaggagttt tatagggat cattctcagc 660  
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 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

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aatgtt						726

&lt;210&gt; 245

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 245

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&lt;210&gt; 246

&lt;211&gt; 821

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 246

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gacaaaccan	gaaactgaag	cctgcctnat	taagtttccg	t		821

&lt;210&gt; 247

&lt;211&gt; 639

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 247

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&lt;210&gt; 248

&lt;211&gt; 846

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 248

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&lt;210&gt; 249

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 249

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&lt;210&gt; 250

&lt;211&gt; 899

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 250

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&lt;210&gt; 251

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 251

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&lt;210&gt; 252

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 252

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753

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<211> 793

<212> DNA

<213> Homo Sapiens

<400> 253

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<211> 625

<212> DNA

<213> Homo Sapiens

<400> 254

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anttccatca gggcttaatc cttca	625

<210> 255

<211> 907

<212> DNA

<213> Homo Sapiens

<400> 255

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ctcaaag						907

&lt;210&gt; 256

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 256

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&lt;210&gt; 257

&lt;211&gt; 885

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 257

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&lt;210&gt; 258

&lt;211&gt; 798

&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

&lt;400&gt; 258

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&lt;210&gt; 259

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 259

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&lt;210&gt; 260

&lt;211&gt; 772

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 260

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&lt;211&gt; 661

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 264

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&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 265

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&lt;210&gt; 266

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 266

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&lt;210&gt; 267

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 267

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&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 268

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&lt;210&gt; 269

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 269

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&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 270

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&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 271

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&lt;211&gt; 862

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 274

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<211> 805  
<212> DNA  
<213> Homo Sapiens

<400> 277  
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gtcctctcatt ttcttgaaga agaatctcag cctgaaagaa tatagagcta ggtgacatat 180  
gggtggccaa ccgcttctcc tcaagttcca agagagtggg caattagtga aattccatca 240  
gtcatgttaa aatatacttt caccaggtag acatccttct ttcaatgcta gaggacagtg 300

aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
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&lt;210&gt; 278

&lt;211&gt; 1358

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 278

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&lt;210&gt; 279

&lt;211&gt; 702

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 279

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caactccaaa	atatcattga	ggctaattct	cagcattacc	aaaaaaatat	taatagtttg	240
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gagaacttag	taaaacaatg	tgaggcaagt	gaaaagaaca	tccagaagaa	atatgaatgt	420
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&lt;210&gt; 280

&lt;211&gt; 874

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 280

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ggaatcctan	attttacagg	ggggaaaaaa	aaacacnaaa	caaaacaaaa	accagaatca	540
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gnettaccaa	aatactaanc	ctttccccaa	aacc			874

&lt;210&gt; 281

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 281

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ttaaagggtg						730

&lt;210&gt; 282

&lt;211&gt; 699

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 282

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&lt;210&gt; 283

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 283

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&lt;210&gt; 284

&lt;211&gt; 764

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 284

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&lt;210&gt; 285

&lt;211&gt; 586

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 285

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ttcaagtttt	ggtacagaag	tatacattca	actatgagtg	ccacgttttc	ccatcaaaca	300
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tttggtngcc	ttttncanaa	aatcccattc	natcacaaaa	ccctaaaaag	ccttcttcgt	540
nggggggaaa	aaananactg	ccaaangcaa	aaacaaaaac	ncccaa		586

&lt;210&gt; 286

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 286

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attttt						666

&lt;210&gt; 287

&lt;211&gt; 782

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 287

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aa						782

&lt;210&gt; 288

&lt;211&gt; 707

&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 288

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gaaaatccta	aattcangan	tcctacagaa	gcagagattg	atgctca		707

## &lt;210&gt; 289

## &lt;211&gt; 673

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 289

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gtcgttttta	aaacgtcntg	acgggggaaa	accctggngt	taccaactta	atcccccttg	660
caacaaatnc	ccc					673

## &lt;210&gt; 290

## &lt;211&gt; 573

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 290

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gtagggtctt	atgttgagc	catcatctgt	acgaattctt	canagttgac	ttgtccgtct	120
ccatcaatat	ctgcttcnct	gatcatttca	tctacttctt	catctgtag	tttttcnccn	180
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## &lt;210&gt; 291

## &lt;211&gt; 819

## &lt;212&gt; DNA



## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 291

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agattctgaa	tgctgttaca	gttcacgaga	aactgtccat	actcatcctc	ctgggcccct	420
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ggttgctgan	gtaaaccctg	aanacggggc	tggttnaggg	cgccctcctg	cacatgccct	720
gcatactgtg	gtggcctcat	ccacggnena	aaccanggta	aggcaaggcc	catgatgcca	780
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## &lt;210&gt; 292

## &lt;211&gt; 664

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 292

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ggggaaccca	ctgtctctcg	cattgagcaa	tgcaaaccctc	acaagaggcc	tgtgtgtggc	180
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tggttggaan	ctgagatcat	tccagatggc	tggttctcta	aaggcagcaa	ctacagtga	420
atcctagaca	agtattttta	agaactttga	taatggtgat	tctcgcctgg	actccaagtg	480
aattcctgaa	gtttgtggga	acangaatga	aactgccatc	aatattacaa	cgtttccagn	540
accaagggag	aacaacaagt	ttgcctaang	ggactccggg	ngttgatgcc	tctcaatttg	600
aactggtctg	gatgaaaaat	gcctgatttg	gnaattnaag	cttcccaant	agtttnccca	660
aatg						664

## &lt;210&gt; 293

## &lt;211&gt; 719

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 293

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aacagaaact	tgtttanatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggtgtaaag	180
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gcagaactca	agaagaatgt	ggatttgctc	ttggganntc	aatgttgagc	ggtanantaa	600
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 <211> 762  
 <212> DNA  
 <213> Homo Sapiens

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 ggctgtgtg tggcagtaat ggcaagacct acctcaacca ctgtgaactg catcgagatg 180  
 cctgcctcac tggatccaaa atccagggtg attacgatgg aactgcaaa gagaagaaat 240  
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 gtcgcatcat ccagtggtg gaagctgaga tcattccaga tggctggttc tctaaaggca 360  
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 cgtatccaga ccaggagaac aacaaagttg cttaggggac tctgtgttga tgcctcatt 540  
 gaactgtctg gatgaaaatg ctgattggnat actcagcttc caagagtctc tcaaagtgc 600  
 ctcaaaccca tctttcaacc ctctgagaa agaagtgtgc cctgngaggg attaaacgta 660  
 atgcagatgg agnctgagac cnaaggtgga ccngttnacc gcctgtgtcc ggtgcccggt 720  
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<210> 295  
 <211> 708  
 <212> DNA  
 <213> Homo Sapiens

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 aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180  
 gaaagacatt cagactgggc cacgtgggct tgtagcagg cagaggaacc ctgctttcca 240  
 aaaactgata tagtccagag tcacggcatg tgggaatgtt tccatggaca ctggatctta 300  
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 ctaagcccta tgcttttaga gggctgaagg aaccaaacct agtttaatcc tgtttgtttg 420  
 ctccatgcaa aactttatgg aagactcccc agactaggct atttagcagc ttccatgaat 480  
 ggtcctcaga tcatgtgatt ctacggcata gacgacagct gccctattta cacagaagct 540  
 gcagaactca agaggaatgt ggatttgctc ttgggagttc aatgttgagc ggtaaaagta 600  
 gtctggatg ataaccatgt tccaaatgac taagtgaaga gacactgtgg gttcctgcct 660  
 ttttaacaaa tgggggtact cctgccctc ctcccanaa atgtccaa 708

<210> 296  
 <211> 652  
 <212> DNA  
 <213> Homo Sapiens

<400> 296  
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 aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180  
 gaaagacatt cagactgggc cacgtgggct tgtagcagg cagaggaacc ctgctttcca 240  
 aaaactgata tagtccagag tcacggcatg tgggaatgtt tccatggaca ctggatctta 300  
 acagatgcta tagtgtttac aaaactacac acacagagaa agcccaagga agcctgcagg 360  
 ctaagcccta tgcttttaga gggctgaagg aaccaaacct agtttaatcc tgtttgtttg 420  
 ctccatgcaa aactttatgg aagactcccc aagactaggc tatttagcag cttccatgaa 480  
 tggctcctcag atcaagtgat tctacggnat anacgacaag ctgccctatt tacacagaag 540  
 ctgcangaac tcaagaggga atgtgggatt gccctgggg agttcaatgg ttgcangggg 600

aaaagttant cttgggntga ataaccaggt ttctaaaatg accaaattga aa

652

<210> 297

<211> 879

<212> DNA

<213> Homo Sapiens

<400> 297

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caagttaaat	gcaatataga	agcctactaa	atacaaatac	aagttcacia	acacatatgc	120
aacagaaact	tgtagatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggtgtaaag	180
gaaagacatt	cagactgggc	cacgtgggct	tgtagcagg	cagaggaacc	ctgctttcca	240
aaaactgata	tagtccagag	tcacggcatg	tggaatgtt	tccatggaca	ctggatctta	300
acagatgcta	tagtggttac	aaanctacac	acacagagaa	agcccaagga	agcctgcagg	360
ctaagcccta	tgcttttaga	gggctgaagg	aaccaaacct	agtttaatcc	tgtttgtttg	420
ctccatgcaa	aactttatgg	aagactcccc	agactaggct	atttagcagc	ttccatgaat	480
ggctctcaga	tcatgtgatt	ctacggcata	gacgacagct	gccctattta	cacagaagct	540
gcagaactca	agaggaatgt	ggatttgctc	ttgggagttc	aatgttgacg	ggtagaagta	600
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ctttgattaa	aggcgtgctg	cctgttgagt	tcccaangg	nacttgggac	anggganccg	780
catttcaaga	ccggaacaaa	ttgggagttt	tgaaaaaagt	ttttaaatng	ggaatgggtt	840
acataaaaaan	gcttgaaatg	gctaaaacaa	agnggggaa			879

<210> 298

<211> 697

<212> DNA

<213> Homo Sapiens

<400> 298

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aaggacatag	ctttggaacc	taaggaacaa	aaacatgaag	acaggcagag	caatacacct	180
tctcctcctg	ttagtacctt	ttcatcaggt	acttctacca	ccagtgatat	tgaagtttta	240
gatcatgaaa	gtgtaataag	tgagagctca	gcgagctcga	gacaagagac	tacagattca	300
aaatcaagtc	ttcacttgat	gcagacatct	tttcagcttc	tctctgcac	tgcttgctct	360
gaatataatc	gttagatga	tttccaaaaa	ctcactgaga	gttgctgttc	atctgatgct	420
tttgaaagaa	tagactcatt	tagtgtacag	tcattagata	gccggagtgt	aagtgaatc	480
aattcaagat	gatgaattgt	caggcaaggg	gatatgcttt	agtgcctatt	ataagttaat	540
tcttcaactc	caaaagtcta	aaacagttga	atctgccgaa	ggaaaatctg	aagaagtaaa	600
tgaaacatta	agttatacca	ctgaggaagc	agaaatggga	agaaaagtgg	gcgaaagtgg	660
caactccccg	gttaacngng	aaaangcctg	gatatcc			697

<210> 299

<211> 510

<212> DNA

<213> Homo Sapiens

<400> 299

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aatacttcnt	ccaaatcntt	taaatgttnt	naangccntt	gcnaaatcct	tataaataaa	120
ttttncct	tatccaancn	catcnanaaa	acattgaata	tgttcaggtt	tcnnggann	180
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ttccnatcna	aatttttttt	aagtttaaat	cnttccnctn	ttaaatttcn	nanagtgtcc	300
gtgtactcc	tacttttaaa	ggaaaaaaat	tantttaaaa	tttaatancc	cccatttaa	360

taattttt	ctttaacn	cn. taatgtt	cnt tttcctga	ac nntaatta	aan aaatgttg	aa	420
attttaaat	g tnaaanant	c caantttc	cg tntgttaa	ca ttacncct	cc aatgttcn	ta	480
atata	tn	ta	cc	cn	ta	at	510

<210> 300  
 <211> 625  
 <212> DNA  
 <213> Homo Sapiens

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tgcttttagt	g cctattat	ag ttaattct	tc aactccaa	ag tctaaaac	cag ttgaatc	tg	120
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ggaagaaagt	ggacgaagt	g caactcct	gt taactgt	gaa cagcctg	ata tcttggt	ttc	240
ttctacacca	ataaatga	ag gacagact	gt gttagaca	ag gtggctg	anc agtgtga	acc	300
tgctgaaagt	cagccana	an cactttct	ga caaggaan	at gtttgca	ata cagttga	att	360
tctgaatgaa	aaagcngg	aa aaaaggg	ang ctcagtt	att atctctt	agt aaggaaa	ag	420
cacttctagg	aagaagctt	tt ttgatac	ctg aananat	gaa atgttcac	ag tngaaagg	aa	480
naanngcagt	ancatttcc	n tccttgaa	an gattnngt	ttt actcaa	agg attngnn	aa	540
nccngtanta	gaaaagt	ttc aaaccta	agn ccggnaaa	ag aggaaga	gat gcctggc	cta	600
aaaaaaggga	aatccacn	ga ccatt					625

<210> 301  
 <211> 792  
 <212> DNA  
 <213> Homo Sapiens

<400> 301							
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tttntctccat	tatccaatca	catctaaa	ata acattga	ata tntacag	gtt nctctgg	ata	180
ggtaccaaaaa	ggtaccacnt	tttataca	aaa cttaatt	gtg aaanctg	gggt gaaataa	aatt	240
tncaaatcaa	aatttttttt	aa aanttt	aaat catncac	tct ttaaatt	tca aacagt	gtca	300
gtgtgacnct	tactttttaa	aa ggaaaaa	aat tagttt	aaaa tttaat	ancc acanatt	taa	360
taatttttta	ctttaacact	taaatgtac	at tttcat	ganc agtaatt	aaa atatnt	tga	420
attttaaatn	tgaaaaat	ttt caaagt	ttca gtatnt	ttaac attacn	ctc aaatgt	tct	480
aatatatata	taaacactta	caaattata	aa atacaac	tag ttgtnt	ntct acaata	cata	540
tntgaacacc	attcttcttc	t tctagcca	tn tttatnt	gan gataaa	agtaa taaatc	tct	600
tgctattcaa	gggaaaaaaa	aa atgaat	gctt taaaaa	ata atcttt	aaaa aataat	tcca	660
aaaataaagt	tcaaata	tgt caaaaa	ata attta	actgt aaatatt	act ncntag	tgt	720
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tatgggaaat	cc						792

<210> 302  
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 <212> DNA  
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ttcagatcaa	aatttttttt	aa agtttaa	at cattcac	tct ttaaatt	tca gacagt	gtca	300
gtgtgactct	tactttttaa	aa ggaaaaa	aat tagttt	aaaa tttaat	agcc acagatt	taa	360

taatttttta	ctttaacact	taatgtacat	tttcatgagc	agtaattaag	atatgttgaa	420
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taatataat	ataaacactt	acaaattata	gatacaacta	gttgatatc	tacaatacat	540
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ctgggtgctat	tcaaggnaaa	aaaatggaat	gccttaaaaa	aataaaatcc	ttaaagaata	660
ggttcaaaaa	ataaagttca	aaatantngc	ccaaaaataa	attaacnngg	taatattaac	720
tacataaggg	taaaacaa					738

&lt;210&gt; 303

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 303

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aacnaccang	nagaangaan	tgaaaanacan	cttacatgaa	tccttgacaa	ttggncaant	600
caagaaactt	cctgaaacaa	ctgaaatcac	aaagt			635

&lt;210&gt; 304

&lt;211&gt; 847

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 304

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gacctaa						847

&lt;210&gt; 305

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 305

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&lt;210&gt; 306

&lt;211&gt; 1659

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 306

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tttcttcagt	gcctttctct	cgccaactga	tgtccagacc	attcagaaga	gtccagtggg	540
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&lt;210&gt; 307

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 307

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&lt;210&gt; 308

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 308

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&lt;210&gt; 309

&lt;211&gt; 1320

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 309

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&lt;210&gt; 310

&lt;211&gt; 1030

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 310

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&lt;210&gt; 311

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 311

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cgggcc						546

&lt;210&gt; 312

&lt;211&gt; 518

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens



&lt;400&gt; 312

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&lt;210&gt; 313

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 313

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&lt;210&gt; 314

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 314

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acaaactata caatcttatt	attttaatgc	tggttt			516

&lt;210&gt; 315

&lt;211&gt; 677

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 315

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&lt;210&gt; 316

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 316

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gga						843

&lt;210&gt; 317

&lt;211&gt; 835

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 317

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&lt;210&gt; 318

&lt;211&gt; 582

&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 318

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## &lt;210&gt; 319

## &lt;211&gt; 827

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 319

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## &lt;210&gt; 320

## &lt;211&gt; 598

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 320

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## &lt;210&gt; 321

## &lt;211&gt; 808

## &lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 321

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&lt;210&gt; 322

&lt;211&gt; 629

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 322

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&lt;210&gt; 323

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 323

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798

<210> 324  
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 <212> DNA  
 <213> Homo Sapiens

&lt;400&gt; 324

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<210> 325  
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 <212> DNA  
 <213> Homo Sapiens

&lt;400&gt; 325

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 <212> DNA  
 <213> Homo Sapiens

&lt;400&gt; 326

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&lt;210&gt; 327

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 327

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&lt;210&gt; 328

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 328

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&lt;210&gt; 329

&lt;211&gt; 978

&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

&lt;400&gt; 329

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&lt;210&gt; 330

&lt;211&gt; 1017

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 330

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&lt;210&gt; 331

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 331

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&lt;210&gt; 332

&lt;211&gt; 881

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 332

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&lt;210&gt; 333

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 333

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&lt;210&gt; 334



&lt;211&gt; 808

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 334

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&lt;210&gt; 335

&lt;211&gt; 758

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 335

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&lt;210&gt; 336

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 336

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&lt;210&gt; 337

&lt;211&gt; 643

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 337

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&lt;210&gt; 338

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 338

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&lt;210&gt; 339

&lt;211&gt; 758

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 339

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&lt;210&gt; 340

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 340

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&lt;210&gt; 341

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 341

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&lt;210&gt; 342

&lt;211&gt; 906

&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 342

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## &lt;210&gt; 343

## &lt;211&gt; 875

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 343

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## &lt;210&gt; 344

## &lt;211&gt; 629

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 344

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&lt;210&gt; 348

&lt;211&gt; 862

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 348

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&lt;211&gt; 832

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 349

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<400> 355



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&lt;210&gt; 356

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 356

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&lt;210&gt; 357

&lt;211&gt; 725

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 357

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 <213> Homo Sapiens

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&lt;210&gt; 361

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 361

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&lt;210&gt; 362

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 362

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&lt;211&gt; 1227

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 363

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&lt;210&gt; 364

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 364

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&lt;210&gt; 365

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 365

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 366

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&lt;211&gt; 803

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 367

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&lt;210&gt; 368

&lt;211&gt; 809

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 368

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&lt;211&gt; 826

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 369

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&lt;210&gt; 370

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 370

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&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 374

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&lt;211&gt; 734

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 375

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 376

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&lt;213&gt; Homo Sapiens

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 378

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&lt;213&gt; Homo Sapiens

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&lt;213&gt; Homo Sapiens

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&lt;210&gt; 389

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 389

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&lt;210&gt; 390

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 390

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&lt;210&gt; 391

&lt;211&gt; 776

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 391

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&lt;210&gt; 392

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 392

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agggacctg

909

&lt;210&gt; 393

&lt;211&gt; 769

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 393

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&lt;210&gt; 394

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 394

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&lt;210&gt; 395

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 395

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&lt;210&gt; 396

&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 396

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&lt;210&gt; 397

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 397

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&lt;210&gt; 398

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 398

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&lt;210&gt; 399

&lt;211&gt; 800

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 399

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&lt;210&gt; 400

&lt;211&gt; 810

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 400

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810

&lt;210&gt; 401

&lt;211&gt; 860

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 401

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&lt;210&gt; 402

&lt;211&gt; 779

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 402

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&lt;210&gt; 403

&lt;211&gt; 1443

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 403

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&lt;210&gt; 404

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 404

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&lt;210&gt; 405

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 405

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&lt;211&gt; 758

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 406

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&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 407

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gaagataatt	gcagtgtcta	aaggacactt	agacagatgt	ccttcntatg	gaagaattaa	720
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&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 408

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 <212> DNA  
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## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 411

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## &lt;210&gt; 412

## &lt;211&gt; 857

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 412

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## &lt;210&gt; 413

## &lt;211&gt; 790

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 413

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ggntttaccc	ncttcngttg	gaaataagga	ttcttgatng	actaaannnc	agctggtnaa	660
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aaaangngnt	tttaagttcc	ggtaatccta	ccggnaatta	nttgggggct	ntgaattcan	780
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<210> 416  
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 <212> DNA



## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 416

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tcctgtaaa	aagttcacct	caagctgcag	tgccctataa	aaaagatgtt	gggaaaaccc	540
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## &lt;210&gt; 417

## &lt;211&gt; 880

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 417

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## &lt;210&gt; 418

## &lt;211&gt; 763

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 418

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tagaaattct	tatggactgg	aatcttcttc	aaggcttact	ttgttcctgg	gatgcagtgg	480
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ataatgtgca agttattaaa gacatgagtg aattcgtgac agattgtcag aaaagaaaca	600
agagtttttct acaacaaaaa actggcttat ggaacatata cttctgcttg agttgaatgt	660
gttggggctg agtgttaagaa aatgcaagct gcaaactctg cttacatgtg gaaccaaagc	720
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&lt;210&gt; 419

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 419

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tggattcact acttttttta nagngtcggt ttaccactac tattggccta ttactgtat	180
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ccttccttct tttgtgctat tgatgacnca ttttactcc tacagatatt ataaacaaat	360
tgatatacnc acattatcat ttttgcttta catactcaat tatcttttaa ataaaaataa	420
aattgaggag aaaatccgtt atattatcta cacatttact gtttccagca cttttcattt	480
ctttgngtag attcaaattt ctgncatctt ccctttgccc aaagaacttc ttttcatctt	540
tcttatagtt caggtctgct ggcaaccaat tagctcagcc tttggtttgc taaaaaagtt	600
catatattat cttgattttc aaatggnatt taagctctat ataggaattc ttaggtgact	660
ttaattcctt catcattggg aagangtcac aaagggcttg caaaggacta gaaatctgct	720
tacatttttt natttggtaa tctttcttac cca	753

&lt;210&gt; 420

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 420

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ccaagtgcac acacctgttg ctactgttaa acagactaag gacttgacag acacactgat	720
ggataatatg tcatecttga ccagccttc tggtagtacc cctaaatctt ctgcttcaag	780
tctttcactt ctggtcctt	799

&lt;210&gt; 421

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 421

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aggaaaacca ttgtgtaaaa cagtaggcgg atctttcaga gactccaaat cattgacaat	180

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&lt;210&gt; 422

&lt;211&gt; 733

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 422

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aaccagccc	gaa					733

&lt;210&gt; 423

&lt;211&gt; 862

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 423

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acacnggaaa	ccagcaggcc	cg				862

&lt;210&gt; 424

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 424

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&lt;210&gt; 425

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 425

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&lt;210&gt; 426

&lt;211&gt; 724

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 426

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atcacaggaa	atacagtgca	ttttcaagtt	ggagagacaa	atactttctc	attcacagtg	180
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 <212> DNA  
 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

<400> 428						
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 <212> DNA  
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<400> 429						
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&lt;210&gt; 430

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 430

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&lt;210&gt; 431

&lt;211&gt; 844

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 431

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&lt;210&gt; 432

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 <212> DNA  
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<400> 432

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 <212> DNA  
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<400> 433

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 <212> DNA  
 <213> Homo Sapiens

<400> 434

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 <212> DNA  
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&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 438

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&lt;210&gt; 439

&lt;211&gt; 826

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 439

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&lt;211&gt; 875

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 443

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&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 444

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&lt;210&gt; 445

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 445

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&lt;210&gt; 446

&lt;211&gt; 866

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 446

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&lt;210&gt; 447

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 447

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789

&lt;210&gt; 448

&lt;211&gt; 820

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 448

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&lt;210&gt; 449

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 449

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&lt;210&gt; 450

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 450

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&lt;210&gt; 451

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 451

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&lt;210&gt; 452

&lt;211&gt; 672

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 452

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&lt;211&gt; 740

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 456

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&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 457

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&lt;210&gt; 458

&lt;211&gt; 870

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 458

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&lt;210&gt; 459

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 459

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&lt;210&gt; 460

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 460

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 <212> DNA  
 <213> Homo Sapiens

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aaac						784

&lt;210&gt; 464

&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 464

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&lt;210&gt; 465

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 465

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&lt;210&gt; 466

&lt;211&gt; 1240

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 466

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&lt;210&gt; 467

&lt;211&gt; 885

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 467

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&lt;210&gt; 468

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 468

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&lt;210&gt; 469

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 469

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&lt;210&gt; 470

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 470

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&lt;210&gt; 471

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 471

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&lt;210&gt; 472

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo. Sapiens

&lt;400&gt; 472

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&lt;210&gt; 473

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Homo. Sapiens

&lt;400&gt; 473

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804

&lt;210&gt; 474

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 474

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&lt;210&gt; 475

&lt;211&gt; 721

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 475

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a						721

&lt;210&gt; 476

&lt;211&gt; 442

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 476

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<212> DNA  
<213> Homo Sapiens

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<212> DNA  
<213> Homo Sapiens

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&lt;210&gt; 480

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 480

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&lt;210&gt; 481

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 481

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&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 482

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&lt;210&gt; 483

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 483

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&lt;210&gt; 484

&lt;211&gt; 788

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 484

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&lt;210&gt; 485

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 485

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&lt;210&gt; 486

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 486

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&lt;210&gt; 487

&lt;211&gt; 728

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 487

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&lt;210&gt; 488

&lt;211&gt; 788

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 488

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&lt;210&gt; 489

&lt;211&gt; 875

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 489

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 <213> Homo Sapiens

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&lt;210&gt; 493

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 493

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&lt;210&gt; 494

&lt;211&gt; 856

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 494

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&lt;210&gt; 495

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 495

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&lt;210&gt; 496

&lt;211&gt; 1759

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 496

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&lt;211&gt; 787

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 500

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;211&gt; 626

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 502

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 503

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 505

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## &lt;211&gt; 742

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 506

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&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 508

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 509

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 <213> Homo Sapiens

<400> 512						
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&lt;211&gt; 727

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 513

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&lt;211&gt; 877

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 514

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877

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&lt;211&gt; 685

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 515

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&lt;211&gt; 790

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 516

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&lt;210&gt; 517

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 517

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&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 518

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&lt;210&gt; 519

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 519

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&lt;211&gt; 827

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens



&lt;400&gt; 520

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&lt;210&gt; 521

&lt;211&gt; 710

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 521

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 522

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&lt;210&gt; 523

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 523

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 524

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&lt;211&gt; 847

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 525

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&lt;213&gt; Homo Sapiens

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&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;211&gt; 815

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 537

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&lt;213&gt; Homo Sapiens

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ggaaaagact aactcaaagc ttcaagaaga gctttcagct gcaacagacc gaatttgctc 600  
acttcaagaa gaacagcagc agttaaagag aacnaaatga attaattcga gaaagaagtn 660  
aaaagagtgt agaagatacn aaacaggatc caaagttgag ctggagactt acagccaact 720  
tcgcaaggtc tggatgaaat gtcnntgatg tgtggaagca cttaaagagg agaagaaagt 780  
ccggttggaa ctggaaaaaa gaactggagn tccaaatggg aatgaaaacc caaatnggaa 840  
atgccatgaa gttcctggna aaggccccc ccaa 874

<210> 541  
<211> 729  
<212> DNA  
<213> Homo Sapiens

<400> 541  
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gcatgaatca ggtttttaga aggaaggtag gagaggaaaa ctactcata gcagaactga 180  
actgctgtaa aatagggtta attctttgaa aagtgaaaaa tgatagtagc aaaatcatga 240



agttgtatct	gaaccagagc	cgtgatgtaa	ccaagtaaga	tggaagtttc	catccagagg	300
agttaattcc	gaacaagtca	cagaaaagggtg	agagctgccg	gttccggcac	gctgtcttct	360
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acatttccca	agcccttga	gaccacagc	gtttggcact	gtccgtgagg	ctgtgtctct	480
gaggacggac	gttcaggagg	ccgtggagga	gcagcgtgc	aggagcagg	tgtggcagct	540
gtcgcacact	cgaccggct	tggggtagga	gggcagggcc	cagctcgttg	ctgggagcag	600
gtgtttgcan	aagatgtggc	ccacagtcc	ggcagtnngt	gctttctccg	gggaaaatgg	660
agaacttcct	ttntcacacn	tggctaccag	tggggtcgnt	ttcggcatct	tttcaagcca	720
ggcgtggg						729

&lt;210&gt; 542

&lt;211&gt; 830

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 542

gggacagcgg	ggacggcacg	gcgcgcgcag	cttctaagtg	ccagatgatg	gaggagcgtg	60
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cactcatgca	aaagaaactg	gcagattatc	tgaaagtgt	tatagacaat	aaacatctct	420
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gtctgtcgtg	gggactcaat	gttctcgatg	ccaatctctg	cttgaaagga	gaagacttgg	540
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ttaacccggc	acttgagctg	caccagtggg	ggatctttca	acccaagata	gatggctttg	720
gaaaagacta	actcaagct	tcagaagagc	nttnagctgc	accagaccga	attttgtctc	780
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&lt;210&gt; 543

&lt;211&gt; 733

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 543

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gcatgaatca	ggtttttaga	aggaaggtag	gagaggaaaa	ctactcacta	gcagaactga	180
actgctgtaa	aataggttaa	attctttgaa	aagtgaaaaa	tgatagtagc	aaaatcatga	240
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agttaattcc	gaacaagtca	cagaaaagggtg	anagctgccg	gttccggcac	gctgtcttct	360
ggagtgccag	tgaccgggca	agaaatttga	ttctttcctt	tgattctctt	gggaaagaac	420
acatttccca	agcccttga	gaccacagc	gtttggcact	gtccgtgagg	ctgtgtctct	480
gaggacggac	gttcaggagg	cccgtggagg	agcagcgtg	caggagcagg	gtgtggcagc	540
tgtcgcacac	tcgcaccggc	ttggggtagg	anggcagggc	tagctcgttg	ctggancang	600
tgttgcaaaa	naatgtggcc	acagntncgg	cagtgggtgc	ttntccggg	aaaagggaga	660
acttcttnt	cacacttggc	tacagngng	gncgctttcg	ncatcttttt	anccagggcg	720
nnggcccttt	caa					733

&lt;210&gt; 544

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 544

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agcacagaga gttcagagca aaaactaaca gggatcttga aattaaagat caggaaatag      120
agaaattgag aatagaactg gatgaaagca aacaacactt ggaacaggag cagcagaagg      180
cagccctggc cagagaggag tgcctgagac taacagaact gctgggcgaa tctgagcacc      240
aactgcacct caccagatct gaaatagctc aactcagtca agaaaaaagg tatacatatg      300
ataaattggg aaagttacag agaagaaatg aagaattgga ggaacagtgt gtccagcatg      360
ggagagtaca tgagacgatg aagcaaaggc taaggcagct ggataagcac agccaggcca      420
cagcccagca gctggtgcag ctctcagca agcagaacca gcttctcctg gagaggcaga      480
gcctgtcgga agaggtggac cggtgcgga cccagttacc cagcatgcca caatctgatt      540
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tggagtctga ctctagctga gcagactcct ggtgtatggt ttcagaaatg gcttgaagtt      780
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&lt;210&gt; 545

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 545

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Leu Leu Asp Ala Ser Glu Lys Leu Lys Leu Thr Tyr Glu Glu Lys Cys
 1          5          10          15
Glu Ile Glu Glu Ser Gln Leu Lys Phe Leu Arg Asn Asp Leu Ala Glu
 20          25          30
Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu
 35          40          45
Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
 50          55          60
Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
 65          70          75          80
His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
 85          90          95
Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
100          105          110
Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
115          120          125
Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
130          135          140
Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
145          150          155          160
Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
165          170          175
Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
180          185          190
Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
195          200          205
Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
210          215          220
Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
225          230          235          240
Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
245          250          255

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Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu  
 260 265 270  
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu  
 275 280 285  
 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu  
 290 295 300  
 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Ser  
 305 310 315 320  
 Glu Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu  
 325 330 335  
 Gly Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln  
 340 345 350  
 His Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp  
 355 360 365  
 Lys His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys  
 370 375 380  
 Gln Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp  
 385 390 395 400  
 Arg Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys  
 405 410

<210> 546  
 <211> 2885  
 <212> DNA  
 <213> Homo Sapiens

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 gagcgccccc cctgggagcg ctccctccta caaactgcct ttgcctgggc cctacgacag 180  
 tcgagacgac ttccccctcc gcaaaacagc ctctgaaccc aacttgaaag tgcgttcaag 240  
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 tggtattagc acctttaaga agagagctgt tgagatcaca ggtgccgggc ctggggcgctc 360  
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 gcaccgagcc ctccctctgg acagctcccc caaccagttc agcctctaca cgtctccttc 540  
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aattt

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&lt;210&gt; 547

&lt;211&gt; 897

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 547

```

Glu Phe Leu Leu Ser Lys Ser Lys Glu Pro Thr Pro Gly Gly Leu Asn
 1             5             10             15
His Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser
 20             25             30
Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Pro Pro Gly Thr Pro Pro
 35             40             45
Ser Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe
 50             55             60
Pro Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Val Arg Ser Arg
 65             70             75             80
Leu Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg
 85             90             95
Lys Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile
100             105             110
Thr Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly
115             120             125
Ser Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn
130             135             140
Gly Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln
145             150             155             160
His Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr
165             170             175
Thr Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val
180             185             190
Thr Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln
195             200             205
Gln Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr

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210	215	220
Leu Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu		
225	230	235
Gly Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu		
245	250	255
Leu Gln His Val Leu Leu Leu Glu Gln Ala Arg Gln Gln Ser Thr Leu		
260	265	270
Ile Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg		
275	280	285
Val Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro		
290	295	300
Leu Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu		
305	310	315
Gln Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln		
325	330	335
Lys Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu		
340	345	350
Leu Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Glu Leu		
355	360	365
Thr Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro		
370	375	380
Arg Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu		
385	390	395
Glu Asp Glu Glu Glu Asp Gly Glu Glu Glu Glu Asp Cys Ile Gln Val		
405	410	415
Lys Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu		
420	425	430
Glu Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu		
435	440	445
Gln Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro		
450	455	460
His Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly		
465	470	475
Met Lys Asn Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Ser		
485	490	495
Val Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn		
500	505	510
Thr His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser		
515	520	525
Arg Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly		
530	535	540
Arg Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His		
545	550	555
Thr Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser		
565	570	575
Lys Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro		
580	585	590
Cys Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His		
595	600	605
Ser Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala		
610	615	620
Phe Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg		
625	630	635
Pro Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe		
645	650	655

Phe Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn  
 660 665 670  
 Val Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly  
 675 680 685  
 Thr Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu  
 690 695 700  
 His Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu  
 705 710 715 720  
 Glu Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp  
 725 730 735  
 Thr Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala  
 740 745 750  
 Phe Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val  
 755 760 765  
 Val Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro  
 770 775 780  
 Leu Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg  
 785 790 795 800  
 Gln Leu Met Thr Leu Ala Gly Gly Arg Val Val Leu Ala Leu Glu Gly  
 805 810 815  
 Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser  
 820 825 830  
 Ala Leu Leu Ser Val Lys Leu Gln Pro Leu Asp Glu Ala Val Leu Gln  
 835 840 845  
 Gln Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu  
 850 855 860  
 Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu  
 865 870 875 880  
 Gly Arg Ser Leu Arg Gly Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu  
 885 890 895

Met

<210> 548  
 <211> 1298  
 <212> DNA  
 <213> Homo Sapiens

<400> 548  
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 tgatggagag agaaagcatc naaagcttct ggaagcaatc agttcccttg atggaaagaa 180  
 taggcggaaa ttggctgana ggtctgagc tagtctgaag gtgtcagagt tcaatgtcag 240  
 ttctgaagga tcaggagaaa agctggctct tgcagatctg cttgagcctg ttaaaacttc 300  
 atcttctttg gccactgtga aaaagcaact gagtagagtc anatcaaaga anacagtgga 360  
 gttacctctg aacaaagaag agattgaacg gatccacaga gaatagcatt caataaaacg 420  
 cacaagtcct ctccaaatgg gaccctgtcg tcctgaagaa ccggcaggca gagcagctgg 480  
 tttttcccct ggagaaagag gagccagcca ttgctcccat tgaacatgtg ctcaagtggct 540  
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 cagtgcacaga ccctttactg acccctgtgg aaaaggctc tctccgagcc atgagcctag 660  
 aagaggcaaa gatgcgacga gcagagcttc agagggctcg ggctctgcag tctactatg 720  
 angccaaggc tcgaagagag aagaaaatcn aaagttaaaa gtatcacaaa gtcgtgaaga 780  
 aaggaaaggc caagaaagcc ctaaaagagt ttgagcagct gcggaagggt aatccagctg 840  
 ccgcactaga agaacgaaga aaagaggaaa gaaggaggag gagaaagaag aagaacaagg 900  
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agaggaagaa	taagaaggaa	agaagaaaga	aaaaagtnaa	agaagaagaa	agaaggaaga	1080
aggaaagaag	aggaagaact	nagaagaaga	aagaggagga	agaagaaag	agaataagg	1140
aacnagaaag	aaggagaaga	aagaataaga	agaggaagaa	gaaaaagaag	aaaagaagaa	1200
ggaaagaagg	agaaaaagga	agaaaaaagg	aagaagaaag	tagaaagcgg	aagaaagaaa	1260
agaaagtata	agaaggaaga	agaagaaaga	aggaaaaa			1298

&lt;210&gt; 549

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 549

Ala	Ala	Glu	Met	Thr	Ala	Asn	Arg	Leu	Ala	Glu	Ser	Leu	Leu	Ala	Leu
1				5				10						15	
Ser	Gln	Glu	Glu	Leu	Ala	Asp	Leu	Pro	Lys	Asp	Tyr	Leu	Leu	Ser	Glu
		20					25					30			
Ser	Glu	Asp	Glu	Gly	Asp	Asn	Asp	Gly	Glu	Arg	Lys	His	Lys	Leu	Leu
		35				40					45				
Glu	Ala	Ile	Ser	Ser	Leu	Asp	Gly	Lys	Asn	Arg	Arg	Lys	Leu	Ala	Arg
	50					55				60					
Ser	Glu	Ala	Ser	Leu	Lys	Val	Ser	Glu	Phe	Asn	Val	Ser	Ser	Glu	Gly
65				70				75						80	
Ser	Gly	Glu	Lys	Leu	Val	Leu	Ala	Asp	Leu	Leu	Glu	Pro	Val	Lys	Thr
			85					90					95		
Ser	Ser	Ser	Leu	Ala	Thr	Val	Lys	Lys	Gln	Leu	Ser	Arg	Val	Ser	Lys
			100					105					110		
Thr	Val	Glu	Leu	Pro	Leu	Asn	Lys	Glu	Glu	Ile	Glu	Arg	Ile	His	Arg
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Glu	Ile	Ala	Phe	Asn	Lys	Thr	His	Lys	Ser	Ser	Pro	Asn	Gly	Thr	Leu
	130					135					140				
Ser	Ser	Val	Leu	Lys	Asn	Arg	Gln	Ala	Glu	Gln	Leu	Val	Phe	Pro	Leu
145				150					155					160	
Glu	Lys	Glu	Glu	Pro	Ala	Ile	Ala	Pro	Ile	Glu	His	Val	Leu	Ser	Gly
			165					170					175		
Trp	Lys	Ala	Arg	Thr	Pro	Leu	Glu	Gln	Glu	Ile	Phe	Asn	Leu	Leu	His
		180					185						190		
Lys	Asn	Lys	Gln	Pro	Val	Thr	Asp	Pro	Leu	Leu	Thr	Pro	Val	Glu	Lys
	195					200					205				
Ala	Ser	Leu	Arg	Ala	Met	Ser	Leu	Glu	Glu	Ala	Lys	Met	Arg	Arg	Ala
	210					215					220				
Glu	Leu	Gln	Arg	Ala	Arg	Ala	Leu	Gln	Ser	Tyr	Tyr				
225					230					235					

&lt;210&gt; 550

&lt;211&gt; 2236

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 550

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&lt;210&gt; 551

&lt;211&gt; 652

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 551

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Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
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Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu

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Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val		
145	150	155
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro		
165	170	175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser		
180	185	190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys		
195	200	205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys		
210	215	220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His		
225	230	235
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp		
245	250	255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys		
260	265	270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile		
275	280	285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu		
290	295	300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln		
305	310	315
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu		
325	330	335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu		
340	345	350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu		
355	360	365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu		
370	375	380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg		
385	390	395
Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp		
405	410	415
Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys		
420	425	430
Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile		
435	440	445
Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu		
450	455	460
Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val		
465	470	475
Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile		
485	490	495
Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp		
500	505	510
Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln		
515	520	525
Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu		
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Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln		
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<210> 552
<211> 2162
<212> DNA
<213> Homo Sapiens
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2162

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 <212> PRT  
 <213> Homo Sapiens

<400> 553

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Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100          105          110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115          120          125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130          135          140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145          150          155          160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165          170          175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180          185          190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195          200          205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210          215          220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225          230          235          240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245          250          255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260          265          270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275          280          285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290          295          300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305          310          315          320
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325          330          335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340          345          350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355          360          365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu

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 <211> 493  
 <212> PRT  
 <213> Homo Sapiens

<400> 555  
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 Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu  
 35 40 45

Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu  
 50 55 60  
 Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val  
 65 70 75 80  
 His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met  
 85 90 95  
 Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg  
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 145 150 155 160  
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 Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser  
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 Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln  
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 260 265 270  
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu  
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 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu  
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 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln  
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 Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala Gln  
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 Ala Leu Gln Ala Gln Gln Arg Glu Gln Glu Leu Thr Gln Lys Ile Gln  
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 Gln Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln Tyr Leu Leu  
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 Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His  
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 Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys  
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 His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln  
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485

490

<210> 556  
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 <213> Homo Sapiens

&lt;400&gt; 556

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gctttggggg actccttctt tgaaccctaa taagacccca ctggagtctc tctctctcca     1200
tccctctcct ctgcctctg ctctaattgc tgccaggatt gtcactcaa accttactct     1260
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<210> 557  
 <211> 328  
 <212> PRT  
 <213> Homo Sapiens

&lt;400&gt; 557

```

Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu Met Glu Arg Gln
 1          5          10          15
Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu Asn Glu Arg Tyr
 20          25          30
Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu Lys Phe Lys Lys
 35          40          45
Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu Leu Leu Pro Lys
 50          55          60
Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg Lys Pro Lys Tyr
 65          70          75          80
Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp Asp Leu Asp Gly
 85          90          95
Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys Tyr Glu Glu Gly
100          105          110
Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile Met Gly Lys Asp
115          120          125
Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu Asp Leu Ala Leu
130          135          140

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Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val Val Ser Ala Val  
 145 150 155 160  
 Tyr Glu Arg Gly Ala Glu Arg His Gly Gly Ile Val Lys Gly Asp  
 165 170 175  
 Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp Tyr Thr Leu Ala  
 180 185 190  
 Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln Gly Gly Asp Trp  
 195 200 205  
 Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu Tyr Asp Asp Glu  
 210 215 220  
 Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln Ile His Ala Leu  
 225 230 235 240  
 Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr Lys Pro Arg Thr  
 245 250 255  
 Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp His Pro Trp Asp  
 260 265 270  
 Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu Ala Leu Asn Gln  
 275 280 285  
 Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu Gly Gln Cys Gly  
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 Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu Lys Asp Pro Asp  
 305 310 315 320  
 Ser His Ser Phe Pro Leu Ala Gln  
 325

<210> 558  
 <211> 2289  
 <212> DNA  
 <213> Homo Sapiens

<400> 558  
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 ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180  
 gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tctgaggaga cctgaagctg 240  
 gtcacatcatg aacccagccg tctgcctctg ttgatgcca ttcggccgct gatccactg 300  
 aagcaccagg tggaaataga tcagctgacc ccccgccgct ccaggaagct gaaggaggtg 360  
 cgtctggacc gtctgcaccc cgaaggcctc ggctgagtg tgctggttg cctggagttt 420  
 ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480  
 caggtagggg acgagatcgt ccgatcaat ggatattcca tctcctcctg taccatgag 540  
 gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagttag acacatcggc 600  
 ctgatccccg tgaaaagctc tctgatgag cccctcactt ggcagtatgt ggatcagttt 660  
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 gaacctgagc tcgagcccgc agatgacctg gatggaggca cggaggagca gggagagcag 1380  
 ccacaggaga tgttgaagag gatggtggtt tatcaagaca gcattcaaga caagatttcc 1440

```

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gatggcatcc ttgggacctg aatctatcac ccaggaatct caaactccct ttggccctga 1980
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attgtcactc caaaccttac tctgagctca ttaataaaat aaacagattt attttccagc 2280
ttaaaaaaa 2289

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&lt;210&gt; 559

&lt;211&gt; 481

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 559

```

Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
 1          5          10         15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
 20         25         30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35         40         45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50         55         60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65         70         75         80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85         90         95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100        105        110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
115        120        125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
130        135        140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145        150        155        160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
165        170        175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
180        185        190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
195        200        205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210        215        220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225        230        235        240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245        250        255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys

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	260		265		270										
Glu	Ala	Val	Asn	Val	Leu	Lys	Asn	Ser	Arg	Ser	Leu	Thr	Ile	Ser	Ile
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Val	Ala	Ala	Ala	Gly	Arg	Glu	Leu	Phe	Met	Thr	Asp	Arg	Glu	Arg	Leu
	290						295					300			
Ala	Glu	Ala	Arg	Gln	Arg	Glu	Leu	Gln	Arg	Gln	Glu	Leu	Leu	Met	Gln
305					310					315				320	
Lys	Arg	Leu	Ala	Met	Glu	Ser	Asn	Lys	Ile	Leu	Gln	Glu	Gln	Gln	Glu
			325						330					335	
Met	Glu	Arg	Gln	Arg	Arg	Lys	Glu	Ile	Ala	Gln	Lys	Ala	Ala	Glu	Glu
			340						345					350	
Asn	Glu	Arg	Tyr	Arg	Lys	Glu	Met	Glu	Gln	Ile	Val	Glu	Glu	Glu	Glu
	355						360					365			
Lys	Phe	Lys	Lys	Gln	Trp	Glu	Glu	Asp	Trp	Gly	Ser	Lys	Glu	Gln	Leu
	370					375					380				
Leu	Leu	Pro	Lys	Thr	Ile	Thr	Ala	Glu	Val	His	Pro	Val	Pro	Leu	Arg
385					390					395					400
Lys	Pro	Lys	Tyr	Asp	Gln	Gly	Val	Glu	Pro	Glu	Leu	Glu	Pro	Ala	Asp
			405						410					415	
Asp	Leu	Asp	Gly	Gly	Thr	Glu	Glu	Gln	Gly	Glu	Gln	Pro	Gln	Glu	Met
			420					425					430		
Leu	Lys	Arg	Met	Val	Val	Tyr	Gln	Asp	Ser	Ile	Gln	Asp	Lys	Ile	Ser
	435						440					445			
Gly	Asn	Met	Arg	Lys	Ala	Leu	Thr	Pro	Thr	Leu	Cys	Ser	Pro	Gln	Ser
	450					455					460				
Arg	Ser	Trp	Gly	Arg	Met	Ser	Gly	Ser	Tyr	Ala	Ser	Arg	Arg	Arg	Asp
465					470					475				480	
Pro															

&lt;210&gt; 560

&lt;211&gt; 2409

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 560

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cagcgtgagc	tgacgcggca	ggagcttctc	atgcagaagc	ggctggcgat	ggagtccaac	1080
aagatcctcc	aggagcagca	ggagatggag	cggcaaagga	gaaaagaaat	tgcccagaag	1140

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ccactggagt ctctctctct ccatccctct cctctgcct ctgctctaatt tgctgccagg 2340
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ttaaaaaaa 2409

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<210> 561  
 <211> 521  
 <212> PRT  
 <213> Homo Sapiens

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<400> 561
Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
 1           5           10          15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
          20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
          35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
          50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
          65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
          85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
          100         105         110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
          115         120         125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
          130         135         140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
          145         150         155         160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
          165         170         175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
          180         185         190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
          195         200         205

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Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys  
 210 215 220  
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His  
 225 230 235 240  
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp  
 245 250 255  
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys  
 260 265 270  
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile  
 275 280 285  
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu  
 290 295 300  
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln  
 305 310 315 320  
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu  
 325 330 335  
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu  
 340 345 350  
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu  
 355 360 365  
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu  
 370 375 380  
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg  
 385 390 395 400  
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp  
 405 410 415  
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Thr Phe Cys Pro  
 420 425 430  
 Ser Pro Gln Pro Pro Arg Gly Pro Gly Val Ser Thr Ile Ser Lys Pro  
 435 440 445  
 Val Met Val His Gln Glu Pro Asn Phe Ile Tyr Arg Pro Ala Val Lys  
 450 455 460  
 Ser Glu Val Leu Pro Gln Glu Met Leu Lys Arg Met Val Val Tyr Gln  
 465 470 475 480  
 Asp Ser Ile Gln Asp Lys Ile Ser Gly Asn Met Arg Lys Ala Leu Thr  
 485 490 495  
 Pro Thr Leu Cys Ser Pro Gln Ser Arg Ser Trp Gly Arg Met Ser Gly  
 500 505 510  
 Ser Tyr Ala Ser Arg Arg Arg Asp Pro  
 515 520

&lt;210&gt; 562

&lt;211&gt; 1445

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 562

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 accacgtcgt gaaactaaaa caggaaatca gtttgctcca ggcgagggtc tccaacttcc 360  
 agcgagagaa tgaagccctg cgggtgcggc aggggtgccag cctgaccgtg gtgaagcaga 420  
 acgccgacgt ggcctgcag aacctccggg tggatcatgaa cagtgcacag gcttccatca 480

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cctcagccag ttcttggcca ccacaatggg agcagccctg gccgagttgt ctctgtggtt 780
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tcacc 1445

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<210> 563  
 <211> 192  
 <212> PRT  
 <213> Homo Sapiens

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<400> 563
Pro Ala Gly Ser Pro Ser Ala Asp Phe Ala Val His Gly Glu Ser Leu
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Gly Asp Arg His Leu Arg Thr Leu Gln Ile Ser Tyr Asp Ala Leu Lys
20     25     30
Asp Glu Asn Ser Lys Leu Arg Arg Lys Leu Asn Glu Val Gln Ser Phe
35     40     45
Ser Glu Ala Gln Thr Glu Met Val Arg Thr Leu Glu Arg Lys Leu Glu
50     55     60
Ala Lys Met Ile Lys Glu Glu Ser Asp Tyr His Asp Leu Glu Ser Val
65     70     75     80
Val Gln Gln Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val
85     90     95
Lys Ala Glu Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu
100    105    110
Gln Ala Gln Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys
115    120    125
Gly Gln Gly Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala
130    135    140
Leu Gln Asn Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys
145    150    155    160
Gln Leu Val Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu
165    170    175
Lys Ser Ile Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
180    185    190

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<210> 564  
 <211> 1226  
 <212> DNA  
 <213> Homo Sapiens

<400> 564

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actactgagg ttccctgccc tacctggcgt cctggtccag gggagccctg ggcagaagcc      1020
cccgccccct aaacatagtt tatgtttttg gccacccgca ccgcttccc caagttctgc      1080
tggtggactc tggactgttt cccctctcag catcgctttt gctgggcccgt gattgtcccc      1140
tttgtgggct ggaaaagcag gtgaggggtg gctgggctga ggccattgcc gccactatct      1200
gtgtaataaa atccgtgagc acgaaa      1226

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&lt;210&gt; 565

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 565

```

Met Lys Gly Lys Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly
 1           5           10           15
Gly Gly Ser Pro Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln
 20           25           30
Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Ala Cys
 35           40           45
Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr
 50           55           60
Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu
 65           70           75           80
Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala
 85           90           95
His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu
100          105          110
Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg
115          120          125
Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Lys
130          135          140
Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu
145          150          155          160
Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala Glu Arg Glu Arg Glu
165          170          175
Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp Glu Asp Asp Ser His
180          185          190
Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys His Asp Lys Tyr Met
195          200          205
Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp Glu Lys Arg Lys Lys

```

210	215	220
Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile Ser Phe Glu Leu Met		
225	230	235
Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp		240
	245	250
Ile Glu Glu His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Gly		255
	260	265
Ser Pro Leu Thr Gln Glu Gln Phe Ile Pro Asn Leu Ala Met Lys Glu		270
	275	280
Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr		285
	290	300

<210> 566  
 <211> 1857  
 <212> DNA  
 <213> Homo Sapiens

<400> 566

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aactgaagct	tctctgcacc	actggactta	aggaanagt	tactcgtagg	cggacagctt	120
tagtggccgg	ccggccgctc	tcatccccc	taaggagcag	agtcctttgt	actgaccaag	180
atgagcaaca	tctacatcca	ggagcctccc	acgaatggga	aggttttatt	gaaaactaca	240
gctggagata	ttgacataga	gttgtggtcc	aaagaagctc	ctaaagcttg	cagaaatttt	300
atcccaactt	tgtttggaag	cttattatga	caataccatt	tttcatagag	ttgtgcctgg	360
tttcatagtc	caaggcggag	atcctactgg	cacagggagt	ggtggagagt	ctatctatgg	420
agcgccattc	aaagatgaat	ttcattcacg	gttgcgtttt	aatcggagag	gactggttgc	480
catggcaaat	gctggttctc	atgataatgg	cacccacttt	ttcttcacac	tgggtcgagc	540
agatgaactt	aacaataagc	ataccatctt	tggaaagggt	acaggggata	cagtatataa	600
catgttgcga	ctgtcagaag	tagacattga	tgatgacgaa	agaccacata	atccacacaa	660
aataaaaagc	tgtgaggttt	tgtttaatcc	ttttgatgac	atcattccaa	gggaaattaa	720
aaggctgaaa	aaagagaaac	cagaggagga	agtaaagaaa	ttgaaacca	aaggcacaaa	780
aaattttagt	ttactttcat	ttggagagga	agctgaggaa	gaagaagagg	aagtaaatcg	840
agttagtcat	agcatgaagg	gcaaaagcaa	aagtagtcat	gacttgctta	aggatgatcc	900
acatctcagt	tctgttccag	ttgtagaaag	tgaaaaaggt	gatgcaccag	atttagttga	960
tgatggagaa	gatgaaagt	cagagcatga	tgaatatatt	gatggtgatg	aaaagaacct	1020
gatgagagaa	agaattgcc	aaaaattaaa	aaaggacaca	agtgcgaatg	ttaaatcagc	1080
tggagaagga	gaagtggaga	agaaatcagt	cagccgcagt	gaagagctca	gaaaagaagc	1140
aagacaatta	aaacgggaac	tcttagcagc	aaaacaaaaa	aaagtagaaa	atgcagcaaa	1200
acaagcagaa	aaaagaagt	aagaggaaga	agccctcca	gatggtgctg	ttgccgaata	1260
cagaagagaa	aagcaaaagt	atgaagcttt	gaggaagcaa	cagtcaaaga	agggaaacttc	1320
cgggaagat	cagacccttg	cactgctgaa	ccagttaaaa	tctaaactca	ctcaagcaat	1380
tgctgaaaca	cctgaaaatg	acattcctga	aacagaagta	gaagatgatg	aaggatggat	1440
gtcacatgta	cttcagtttg	aggataaaa	cagaaaagt	aaagatgcaa	gcattgcaaga	1500
ctcagatata	tttgaaatct	atgatcctcg	gaatccagtg	aataaaagaa	ggagggaaga	1560
aagcaaaaag	ctgatgagag	agaaaaaaga	aagaagataa	aatgagaata	atgataacca	1620
gaacttgctg	gaaatgtgcc	tacaatggcc	ttgtaacagc	cattgttccc	aacagcatca	1680
cttaggggtg	tgaaaagaag	tatttttgaa	cctgttgtct	ggttttgaaa	aacaattatc	1740
ttgttttgca	aattgtggaa	tgatgtaagc	aaatgctttt	ggttactggg	acatgtgttt	1800
tttctagct	gaccttttat	attgctaaat	ctgaaataaa	ataactttcc	ttccaaa	1857

<210> 567  
 <211> 372  
 <212> PRT  
 <213> Homo Sapiens

&lt;400&gt; 567

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Met Ala Asn Ala Gly Ser His Asp Asn Gly Thr His Phe Phe Phe Thr
 1           5           10           15
Leu Gly Arg Ala Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys
           20           25           30
Val Thr Gly Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp
           35           40           45
Ile Asp Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys
           50           55           60
Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys
65           70           75           80
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys Pro
           85           90           95
Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu Ala Glu
           100          105          110
Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met Lys Gly Lys
           115          120          125
Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro His Leu Ser Ser
           130          135          140
Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala Pro Asp Leu Val Asp
145           150          155          160
Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu Tyr Ile Asp Gly Asp
           165          170          175
Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys Lys Leu Lys Lys Asp
           180          185          190
Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly Glu Val Glu Lys Lys
           195          200          205
Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu Ala Arg Gln Leu Lys
           210          215          220
Arg Glu Leu Leu Ala Ala Lys Gln Lys Lys Val Glu Asn Ala Ala Lys
225           230          235          240
Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala
           245          250          255
Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys
           260          265          270
Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu
           275          280          285
Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro
           290          295          300
Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met
305           310          315          320
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp Ala
           325          330          335
Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg Asn Pro
           340          345          350
Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met Arg Glu Lys
           355          360          365
Lys Glu Arg Arg
           370

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&lt;210&gt; 568

&lt;211&gt; 1537

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 568

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gccgcgcgcc gatcggtcgt taccgcgagg cgctgggtggc cttcaggctg gacggcgcg 60
gtcagccctg gttcgccggc ttctgggtct ttgaacagcc gcgatgtcga tcttcacccc 120
caccaaccag atccgcctaa ccaatgtggc cgtgggtacgg atgaagcgtg ccgggaagcg 180
cttcgaaatc gcctgctaca aaaacaaggc cgtcgggtcg cggagcggcg tggaaaaaga 240
cctcgatgaa gttctgcaga cccactcagt gtttgtaaag gtttctaaag gtcagggttc 300
caaaaaggaa gatctcatca gtgcgtttgg aacagatgac caaactgaaa tctgtaagca 360
gattttgact aaaggagaag ttcaagtatc agataaagaa agacacacac aactggagca 420
gatgtttagg gacattgcaa ctattgtggc agacaaatgt gtgaatcctg aaacaaagag 480
accatacacc gtgatcctta ttgagagagc catgaaggac atccactatt cggtgaaaac 540
caacaagagt acaaaacagc aggctttgga agtgataaag cagttaaaag agaaaatgaa 600
gatagaacgt gctcacatga agcttcggtt catccttcca gtcaatgaag gcaagaactg 660
aaagaaaagc tcaagccact gatcaaggtc atagaaagtg aagattatgg ccaacagtta 720
gaaatcgatg gtctgattga cccgggctgc ttccgagaaa ttgatgagct aataaaaaag 780
gaaactaaag gcaaagggtt tttggaagta ctcaatctga aagatgtaga agaaggagat 840
gagaaaattg aatgacaccc atcaatctct tcacctctaa aacactaaag tgtttccgtt 900
tccgacggca ctgtttcatg tctgtggtct gccaaatact tgcttaaact atttgacatt 960
ttctatcttt gtgttaacag tggacacagc aaggctttcc tacataagta taataatgtg 1020
ggaatgattt ggttttaatt ataaactggg gtctaaatcc taaagcaaaa ttgaaactcc 1080
aagatgcaaa gtccagagtg gcattttgct actctgtctc atgccttgat agctttccaa 1140
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ttattagggg tatgtctata caacaaaagg gggggtcttt cctaaaaaag aaaacatatg 1260
atgcttcatt tctacttaat ggaacttgtg ttctgagggt cattatggta tcgtaatgta 1320
aagcttgat gatgttctg attatttgag gaacagatat aggaaaattg tgccggaatt 1380
acctttcatt gaacatgctg ccataaatta ggttattttt ggtaaaaaaa taaagtcaa 1440
ttatttttaa tttttaagtt ttataatata tattaatata ggtaaaattg tatgtaatca 1500
ataaaaccaa ttttatgttt attaaactta aaaaaaa 1537

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&lt;210&gt; 569

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 569

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Ala Ala Arg Arg Ser Val Val Thr Ala Arg Arg Trp Trp Pro Ser Gly
1      5      10      15
Trp Thr Ala Arg Val Ser Pro Gly Ser Pro Ala Ser Gly Ser Leu Asn
20     25     30
Ser Arg Asp Val Asp Leu His Pro His Gln Pro Asp Pro Pro Asn Gln
35     40     45
Cys Gly Arg Gly Thr Asp Glu Ala Cys Arg Glu Ala Leu Arg Asn Arg
50     55     60
Leu Leu Gln Lys Gln Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp
65     70     75     80
Leu Asp Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys
85     90     95
Gly Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp
100    105    110
Asp Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln
115    120    125
Val Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp
130    135    140
Ile Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg
145    150    155    160
Pro Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr

```



165 170 175  
 Ser Val Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile  
 180 185 190  
 Lys Gln Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Lys Leu  
 195 200 205  
 Arg Phe  
 210--

<210> 570  
 <211> 1211  
 <212> DNA  
 <213> Homo Sapiens

<400> 570  
 accatctttg gaaagggttac aggggtatcac agtatataac atgttgcgac tgtcagaagt 60  
 agacattgat gatgacgaaa gaccacataa tccacacaaa ataaaaagct gtgaggtttt 120  
 gtttaatect tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 180  
 agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aatttttagtt tactttcatt 240  
 tggagaggaa gctgaggaag aagaggagga agtaaatcga gttagtcaga gcatgaaggg 300  
 caaaagcaaa agtagtcatt acttgcttaa ggatgatcca catctcagtt ctgttcagtt 360  
 tgtagaaagt gaaaaagggtg atgcagcaga tttagttgat gatggagaag atgaaagtgc 420  
 agagcatgat gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 480  
 aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag aagtggagaa 540  
 gaaatcagtc agccgcagtg aagagctcag aaaagaagca agacaattaa aacgggaact 600  
 cttagcagca gaacaaaaaa aagtagaaaa tgacgacaaa caagcagaaa aaagaagtga 660  
 agaggaagaa gccctccag atggtgctgt tgccgaatac agaagagaaa agcaaaagta 720  
 tgaagctctg aggaagcaac agtcaaagaa gggaacttcc cggaagatc agacccttgc 780  
 actgctgaac cagtttaaat ctaaactcac tcaagcaatt gctgaaacgc ctgaaaatga 840  
 cattcctgaa acagaagtag aagatgatga aggatggatg tcacatgtac ttcagtttga 900  
 ggataaaagc agaaaagtga aagatgcaag catgcaagac tcagatacat ttgaaatcta 960  
 tgatcctcgg aatccagtga ataaaagaag gaggaagaa agcaaaaagc tgatgagaga 1020  
 gaaaaaagaa agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1080  
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt gaaaagaagt 1140  
 atttttgaac ctgttgtctg gttttgaaaa acaattatct tgttttgcaa attgtggaat 1200  
 gatgtaagca a 1211

<210> 571  
 <211> 354  
 <212> PRT  
 <213> Homo Sapiens

<400> 571  
 Pro Ser Leu Glu Arg Leu Gln Gly Tyr Thr Val Tyr Asn Met Leu Arg  
 1 5 10 15  
 Leu Ser Glu Val Asp Ile Asp Asp Asp Glu Arg Pro His Asn Pro His  
 20 25 30  
 Lys Ile Lys Ser Cys Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile  
 35 40 45  
 Pro Arg Glu Ile Lys Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val  
 50 55 60  
 Lys Lys Leu Lys Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe  
 65 70 75 80  
 Gly Glu Glu Ala Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln  
 85 90 95  
 Ser Met Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp

100	105	110
Pro His Leu Ser Ser Val	Pro Val Val Glu Ser Glu Lys Gly Asp Ala	
115	120	125
Ala Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu		
130	135	140
Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys		
145	150	155
Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly		
165	170	175
Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu		
180	185	190
Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala Glu Gln Lys Lys Val		
195	200	205
Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala		
210	215	220
Pro Pro Asp Gly Ala Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr		
225	230	235
Glu Ala Leu Arg Lys Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp		
245	250	255
Gln Thr Leu Ala Leu Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala		
260	265	270
Ile Ala Glu Thr Pro Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp		
275	280	285
Asp Glu Gly Trp Met Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg		
290	295	300
Lys Val Lys Asp Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr		
305	310	315
Asp Pro Arg Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys		
325	330	335
Leu Met Arg Glu Lys Lys Glu Arg Arg Ile Leu Pro Val Asn Glu Gly		
340	345	350
Lys Asn		

<210> 572  
 <211> 604  
 <212> DNA  
 <213> Homo Sapiens

<400> 572

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tcccttttagc	aacagggcc	ccaagaagct	ccgttcatt	cacccttacc	ttggccccc	120
ggttggaccc	ccaaaggctc	ccttacccca	aagtgggtg	ttgaataaat	cttctcagtt	180
ccctggctcc	caaggcccat	tgaagaagat	tgtacaaggc	gtgcctcaag	taccccgagt	240
ggaaacagaa	gcacctgcct	cacttcaagc	cgtggctgca	cccggagcag	agcccgttgc	300
cgagcctggc	gctgtcggag	ctgtcgggtg	agcatgcgga	ctcactggag	aacatcgacg	360
agagcgcggt	ggccgagagc	agagaggagc	ggatgggcgg	cgcgggcggc	gagggcagcg	420
acgacgacac	cttcacctga	gcccgccaccg	cttcaggggac	ggagacagga	ccgggcgagc	480
cctggggcgg	cggccgctcc	tgcactttct	cccccccc	acccggcacc	tggtggcacc	540
gggccaggcc	caggcggtg	ctgcagcctg	gctggacaga	gcccataaaa	cggatcccac	600
agcc						604

<210> 573  
 <211> 195  
 <212> PRT

## &lt;213&gt; Homo Sapiens

&lt;400&gt; 573

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Leu Arg Gln Lys Ile Leu Val Pro Thr Phe Cys Ser Ile Pro Lys Gly
 1           5           10           15
Leu Thr Phe Ile Pro Phe Ser Asn Arg Ala Pro Lys Lys Leu Pro Phe
 20           25           30
Ile His Pro Tyr Leu Gly Pro Gln Val Gly Pro Pro Lys Ala Pro Leu
 35           40           45
Pro Gln Ser Gly Trp Leu Asn Lys Ser Ser Gln Phe Pro Gly Ser Gln
 50           55           60
Gly Pro Leu Lys Lys Ile Val Gln Gly Val Pro Gln Val Pro Arg Val
 65           70           75           80
Glu Thr Glu Ala Pro Ala Ser Leu Gln Ala Val Ala Ala Pro Gly Ala
 85           90           95
Glu Pro Val Ala Glu Pro Gly Ala Val Gly Ala Val Gly Ala Ala Cys
100          105          110
Gly Leu Thr Gly Glu His Arg Arg Glu Arg Gly Gly Arg Glu Gln Arg
115          120          125
Gly Ala Asp Gly Arg Arg Gly Arg Arg Gly Gln Arg Arg Arg His Leu
130          135          140
His Leu Ser Pro His Arg Phe Arg Asp Gly Asp Arg Thr Gly Arg Ala
145          150          155          160
Leu Gly Arg Arg Pro Leu Leu His Phe Leu Pro Ser Pro Thr Arg His
165          170          175
Leu Val Ala Pro Gly Gln Ala Gln Ala Gly Ala Ala Ala Trp Leu Asp
180          185          190
Arg Ala Gln
195

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&lt;210&gt; 574

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 574

```

cccaccagg cccctcgat gcagagacag aggtcgggtgc tgaccgctgc acgtcgactg      60
cctaccagga gcagaggccc caggtggagc aagttggcaa agtcgctcct ctctccccag      120
ggctgccggc aatggggggg cctggccccg gccctgtga ggaccccgcg ggtgctgggg      180
gagcaggtgc aggggggtcc gagccccctg tgactgtcac cgtgcagtgc gccttcacag      240
tggccctgag ggcaggaaga ggagccgacc tgtccagcct gcgggcactg ctggggccaag      300
ccttccttca ccaggcccag cttgggcaat tcagttacct agccccaggt gaggacgggc      360
actgggtccc catccccgag gaggagtgcg tgcagagggc ctggcaggac gcagctgcct      420
gccccagggg gctgcagctg cagtgcaggg gagccggggg tcggccggtc ctttaccagg      480
tggtggccca gcacagatac tccgcccagg ggccagagga cctgggcttc cgacaggggg      540
acacggtgga cgtcctgtgt gaagtggacc aggcattggt ggagggccac tgtgacggcc      600
gcacggcat cttccccaag tgcctcgtgg tccccgcgg ccctcggtatg tcaggagccc      660
cggccgcct gcccgatcc cagcagggag atcagcccta atgatgctgt gtccatgatg      720
ctttaataa aaacaacccc ca                                     742

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&lt;210&gt; 575

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 575

His Gln Gly Pro Leu Asp Ala Glu Thr Glu Val Gly Ala Asp Arg Cys  
 1 5 10 15  
 Thr Ser Thr Ala Tyr Gln Glu Gln Arg Pro Gln Val Glu Gln Val Gly  
 20 25 30  
 Lys Val Ala Pro Leu Ser Pro Gly Leu Pro Ala Met Gly Gly Pro Gly  
 35 40 45  
 Pro Gly Pro Cys Glu Asp Pro Ala Gly Ala Gly Gly Ala Gly Ala Gly  
 50 55 60  
 Gly Ser Glu Pro Leu Val Thr Val Thr Val Gln Cys Ala Phe Thr Val  
 65 70 75 80  
 Ala Leu Arg Ala Gly Arg Gly Ala Asp Leu Ser Ser Leu Arg Ala Leu  
 85 90 95  
 Leu Gly Gln Ala Phe Leu His Gln Ala Gln Leu Gly Gln Phe Ser Tyr  
 100 105 110  
 Leu Ala Pro Gly Glu Asp Gly His Trp Val Pro Ile Pro Glu Glu Glu  
 115 120 125  
 Ser Leu Gln Arg Ala Trp Gln Asp Ala Ala Ala Cys Pro Arg Gly Leu  
 130 135 140  
 Gln Leu Gln Cys Arg Gly Ala Gly Gly Arg Pro Val Leu Tyr Gln Val  
 145 150 155 160  
 Val Ala Gln His Arg Tyr Ser Ala Gln Gly Pro Glu Asp Leu Gly Phe  
 165 170 175  
 Arg Gln Gly Asp Thr Val Asp Val Leu Cys Glu Val Asp Gln Ala Trp  
 180 185 190  
 Leu Glu Gly His Cys Asp Gly Arg Ile Gly Ile Phe Pro Lys Cys Phe  
 195 200 205  
 Val Val Pro Ala Gly Pro Arg Met Ser Gly Ala Pro Gly Arg Leu Pro  
 210 215 220  
 Arg Ser Gln Gln Gly Asp Gln Pro  
 225 230

&lt;210&gt; 576

&lt;211&gt; 1087

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 576

aagatgatgc ctagtaaatt acagaagaac aaacagagac tgcgaaacga tcctctcaat 60  
 caaaataagg gtaaaccaga cttgaatata acattgccaa ttagacaaac agcatcaatt 120  
 ttcaaacaac cggtaaccaa agtcacaaat catcctagta ataaagtga atcagaccca 180  
 caacgaatga atgaacagcc acgtcagctt ttctgggaga agaggctaca aggacttagt 240  
 gcatcagatg taacagaaca aattataaaa accatggaac tacccaaagg tcttcaagga 300  
 gttggtccag tagcaatga tgagaccctt ttatctgctg ttgccagtgc tttgcacaca 360  
 agctctgcgc caatcacagg gcaagtctcc gctgctgtgg aaaagaaccc tgctgtttgg 420  
 cttaacacat ctcaaccct ctgcaaagct tttattgtca cagatgaaga catcaggaaa 480  
 caggaagagc gactacagca agtacgcaag aaattggaag aagcactgat ggcagacatc 540  
 ttgtcgcgag ctgctgatac agaagagatg gatattgaaa tggacagtgg agatgaagcc 600  
 taagaatatg atcaggtaac ttctgaccga ctttcccaa gagaaaattc ctagaaattg 660  
 aacaaaaatg tttccactgg cttttgctg taagaaaaaa aatgtaccg agcacataga 720  
 gctttttaat agcactaacc aatgccttt tagatgtatt tttgatgtat atatctatta 780  
 ttcaaaaaat catgtttatt ttgagtccta ggacttaaaa ttagtctttt gtaatatcaa 840  
 gcaggaccct aagatgaagc tgagcttttg atgccaggtg caatttactg gaaatgtagc 900  
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 taaatttccc agttaagat tattgtgact tcaactgtata taaacatatt tttatacttt 1020

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<213> Homo Sapiens

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Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn  
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Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser  
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115 120 125  
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<213> Homo Sapiens

<400> 578  
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<210> 579  
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 <212> PRT  
 <213> Homo Sapiens

<400> 579

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Asp Phe Tyr Val Gln Leu Ile Glu Asp Glu Ala Glu Ile Ser His Leu
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Pro Pro Leu Gln Arg Gly Asp Met Ile Cys Ala Val Phe Pro Glu Asp
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Leu Ser Val Gln Phe Ile Asp Tyr Gly Asn Val Ser Val Val His Thr
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Asn Lys Ile Gly Arg Leu Asp Leu Val Asn Ala Ile Leu Pro Gly Leu
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 Ala Asp Glu His Gly Ile Ile Ala Asp Asp Met Ile Ser Arg Tyr Ala  
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Thr Ala Gln Leu Pro Leu Asp Asp Lys Met Asp Pro Leu Ser Leu Gly		
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Ser Ser Cys Val Glu Ser Phe Asp Asp Gln Arg Arg Met Ser Leu His		
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Leu His Gly Ala Asp Cys Asp Pro Lys Thr Gln Asn Glu Met Asn Ile		
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Cys Glu Glu Glu Phe Val Glu Tyr Lys Asn Arg Asp Ala Ile Ser Ala		
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 <212> DNA  
 <213> Homo Sapiens

<400> 580

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 <213> Homo Sapiens

<400> 581

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 <212> DNA  
 <213> Homo Sapiens

<400> 582

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gtcattttct 3309

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<210> 583  
 <211> 872  
 <212> PRT  
 <213> Homo Sapiens

<400> 583

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Arg Arg Pro Arg Pro Glu Ala Glu Ala Asp Arg Glu Pro Ala Met Ser
 1          5          10          15
Val Val Gly Leu Asp Val Gly Ser Gln Ser Cys Tyr Ile Ala Val Ala
      20          25          30
Arg Ala Gly Gly Ile Glu Thr Ile Ala Asn Glu Phe Ser Asp Arg Cys
      35          40          45
Thr Pro Ser Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val
      50          55          60
Ala Ala Lys Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn
      65          70          75          80
Phe Lys Arg Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys
      85          90          95
Glu Lys Glu Asn Leu Ser Tyr Asp Leu Val Pro Leu Lys Asn Gly Gly
      100          105          110
Val Gly Ile Lys Val Met Tyr Met Gly Glu Glu His Leu Phe Ser Val
      115          120          125
Glu Gln Ile Thr Ala Met Leu Leu Thr Lys Leu Lys Glu Thr Ala Glu
      130          135          140
Asn Ser Leu Lys Lys Pro Val Thr Asp Cys Val Ile Ser Val Pro Ser
      145          150          155          160
Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Leu Asp Ala Ala Gln Ile
      165          170          175
Val Gly Leu Asn Cys Leu Arg Leu Met Asn Asp Met Thr Ala Val Ala
      180          185          190
Leu Asn Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu Asp Glu Lys
      195          200          205
Pro Arg Ile Val Val Phe Val Asp Met Gly His Ser Ala Phe Gln Val
      210          215          220
Ser Ala Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Gly Thr Ala
      225          230          235          240
Phe Asp Pro Phe Leu Gly Gly Lys Asn Phe Asp Glu Lys Leu Val Glu
      245          250          255
His Phe Cys Ala Glu Phe Lys Thr Lys Tyr Lys Leu Asp Ala Lys Ser
      260          265          270
Lys Ile Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys Leu Lys
      275          280          285
Lys Leu Met Ser Ser Asn Ser Thr Asp Leu Pro Leu Asn Ile Glu Cys
      290          295          300
Phe Met Asn Asp Lys Asp Val Ser Gly Lys Met Asn Arg Ser Gln Phe
      305          310          315          320
Glu Glu Leu Cys Ala Glu Leu Leu Gln Lys Ile Glu Val Pro Leu Tyr

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-312-

Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala Gln Ala  
 770 775 780  
 Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu Ile Lys  
 785 790 795 800  
 Thr Lys Ile Lys Glu Leu Asn Asn Thr Cys Glu Pro Val Val Thr Gln  
 805 810 815  
 Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly  
 820 825 830  
 Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe  
 835 840 845  
 Gly Ala Glu Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys  
 850 855 860  
 Asn Ser Val Asn Met Asp Leu Asp  
 865 870

<210> 584  
 <211> 2918  
 <212> DNA  
 <213> Homo Sapiens

<400> 584

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taccagaaag	tgcctctgaa	ggagccagt	ccagccatca	ccaaactggg	cccctccacc	300
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tggaaacccgc	agcaccttct	catcctgcag	gcccagttcg	cctcgagctt	gcgggagacc	1980
acagaaggca	agtacatcat	gtcggacttg	ggcccgcagg	agagggtgca	catctcgaag	2040

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&lt;210&gt; 585

&lt;211&gt; 687

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 585

```

Met Ala Ala Glu Val Ala Leu Ser Glu Ser Ala Lys Asp Gln Lys Ala
 1          5          10          15
Ala Asn Pro Tyr Val Thr Pro Asn Asn Arg Tyr Gly Tyr Gln Asn Gly
 20          25          30
Ala Ser Tyr Thr Trp Gln Phe Glu Ala Arg Lys Ala Gln Ile Leu Lys
 35          40          45
Cys Met Glu Cys Gly Ser Ser His Asp Thr Leu Gln Gln Leu Thr Ala
 50          55          60
His Met Met Val Thr Gly His Phe Leu Lys Val Thr Thr Ser Ala Ser
 65          70          75          80
Lys Lys Gly Lys Gln Leu Val Leu Asp Pro Val Val Glu Glu Lys Ile
 85          90          95
Gln Ser Ile Pro Leu Pro Pro Thr Thr His Thr Arg Leu Pro Ala Ser
100          105          110
Ser Ile Lys Lys Gln Pro Asp Ser Pro Ala Gly Ser Thr Thr Ser Glu
115          120          125
Glu Lys Lys Glu Pro Glu Lys Glu Lys Pro Pro Val Ala Gly Asp Ala
130          135          140
Glu Lys Ile Lys Glu Glu Ser Glu Asp Ser Leu Glu Lys Phe Glu Pro
145          150          155          160
Ser Thr Leu Tyr Pro Tyr Leu Arg Glu Glu Asp Leu Asp Asp Ser Pro
165          170          175
Lys Gly Gly Leu Asp Ile Leu Lys Ser Leu Glu Asn Thr Val Ser Thr
180          185          190
Ala Ile Ser Lys Ala Gln Asn Gly Ala Pro Ser Trp Gly Gly Tyr Pro
195          200          205
Ser Ile His Ala Ala Tyr Gln Leu Pro Gly Thr Val Lys Pro Leu Pro
210          215          220
Ala Ala Val Gln Ser Val Gln Val Gln Pro Ser Tyr Ala Gly Gly Val
225          230          235          240
Lys Ser Leu Ser Ser Ala Glu His Asn Ala Leu Leu His Ser Pro Gly
245          250          255
Ser Leu Thr Pro Pro Pro His Lys Ser Asn Val Ser Ala Met Glu Glu

```

260	265	270
Leu Val Glu Lys Val Thr Gly Lys	Val Asn Ile Lys Lys	Glu Glu Arg
275	280	285
Pro Pro Glu Lys Glu Lys Ser Ser	Leu Ala Lys Ala Ala	Ser Pro Ile
290	295	300
Ala Lys Glu Asn Lys Asp Phe Pro	Lys Thr Glu Glu Val	Ser Gly Lys
305	310	315
Pro Gln Lys Lys Gly Pro Glu Ala	Glu Thr Trp Glu Ala	Lys Lys Glu
325	330	335
Gly Pro Leu Asp Val His Thr Pro	Asn Gly Thr Glu Pro	Leu Lys Ala
340	345	350
Lys Val Thr Asn Gly Cys Asn Asn	Leu Gly Ile Ile Met	Asp His Ser
355	360	365
Pro Glu Pro Ser Phe Ile Asn Pro	Leu Ser Ala Leu Gln	Ser Ile Met
370	375	380
Asn Thr His Leu Gly Lys Val Ser	Lys Pro Val Ser Pro	Ser Leu Asp
385	390	395
Pro Leu Ala Met Leu Tyr Lys Ile	Ser Asn Ser Met Leu	Asp Lys Pro
405	410	415
Val Tyr Pro Ala Thr Pro Val Lys	Gln Ala Asp Ala Ile	Asp Arg Tyr
420	425	430
Tyr Tyr Glu Asn Ser Asp Gln Pro	Ile Asp Leu Thr Lys	Ser Lys Asn
435	440	445
Lys Pro Leu Val Ser Ser Val Ala	Asp Ser Val Ala Ser	Pro Leu Arg
450	455	460
Glu Ser Ala Leu Met Asp Ile Ser	Asp Met Val Lys Asn	Leu Thr Gly
465	470	475
Arg Leu Thr Pro Lys Ser Ser Thr	Pro Ser Thr Val Ser	Glu Lys Ser
485	490	495
Asp Ala Asp Gly Ser Ser Phe Glu	Glu Ala Leu Asp Glu	Leu Ser Pro
500	505	510
Val His Lys Arg Lys Gly Arg Gln	Ser Asn Trp Asn Pro	Gln His Leu
515	520	525
Leu Ile Leu Gln Ala Gln Phe Ala	Ser Ser Leu Arg Glu	Thr Thr Glu
530	535	540
Gly Lys Tyr Ile Met Ser Asp Leu	Gly Pro Gln Glu Arg	Val His Ile
545	550	555
Ser Lys Phe Thr Gly Leu Ser Met	Thr Thr Ile Ser His	Trp Leu Ala
565	570	575
Asn Val Lys Tyr Gln Leu Arg Arg	Thr Gly Gly Thr Lys	Phe Leu Lys
580	585	590
Asn Leu Asp Thr Gly His Pro Val	Phe Phe Cys Asn Asp	Cys Ala Ser
595	600	605
Gln Phe Arg Thr Ala Ser Thr Tyr	Ile Ser His Leu Glu	Thr His Leu
610	615	620
Gly Phe Ser Leu Lys Asp Leu Ser	Lys Leu Pro Leu Asn	Gln Ile Gln
625	630	635
Glu Gln Gln Asn Val Ser Lys Val	Leu Thr Asn Lys Thr	Leu Gly Pro
645	650	655
Leu Gly Ala Thr Glu Glu Asp Leu	Gly Ser Thr Phe Gln	Cys Lys Leu
660	665	670
Cys Asn Arg Thr Phe Ala Lys Gln	Ala Arg Ser Gln Thr	Ala Pro
675	680	685

&lt;210&gt; 586

<211> 1898  
 <212> DNA  
 <213> Homo Sapiens

<400> 586

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tgagtcgga tggggaaggg ccgcccccca ggggtgggctt tgtggacagc accatcaaga      180
gcctggacga naagctgcgg actctgctct accaggagca cgtgcccacc tcctcagcct      240
cagctgggac ccctgtggag gtgggcgaca ganacttcac cctggagccc ctgagagggg      300
accagccccg ctcanaggtc tggggggggg acctggccct gccccagtg cctaaggagg      360
cgggtctcagg gcgtgtccag ctgccccagc ccttgggtga gaagtcagaa ctggccccca      420
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gtatgctagg ctatgacaga gatggaaggc aggtggcctc agactcccat gtggtcccca      540
gcgtcccccna ggatgtacct gcttttgtga gacctgcacg tgtgganccc acanacaggg      600
atggtggana agctgganaa agctcggcan agcccccgcc gactgacatg ggcanngtgg      660
ggggccaggc tagccacccc cagacactcg gcnctcgagc tttgggggtcc cctcggaanc      720
gtccagatca ccaggatgtc agctcaccag ccaagactgt gggccgtttc tcggtgtgta      780
gcactcagga cgagtggacc ctggcctccc cccacagcct gagatactct gccccacccg      840
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tggctggcga cttcgtgaag aaggccaccg cttcctgcag aggccttctc gggccggctt      1080
cgctgggccc cgagacaccc agcagggtgg gcataaggt cccacgacac agcgtgacct      1140
ccttccattc ccagtcgtcc tacatcagca gcgacaatga ttcggagctc gaggatgctg      1200
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cagtgtgggg ctactgcan acaacacggg cctgaacggg aangcagtcg anaccanca      1560
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gcggaacgcg tngncaangg tctccacca acaacctggc ccaggcctga accaagcccc      1680
acccgccctg cagctccaag cgcangtgaa caacancaac nacaagaaag gttcttcncc      1740
gacgaactgc acaantggt ggacnaatgg acaacaanan ngtggggggc gcgactgaa      1800
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<210> 587  
 <211> 399  
 <212> PRT  
 <213> Homo Sapiens

<400> 587

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  1             5             10             15
Ser Leu Ala Thr Ser Gln Leu Pro Ser Pro Pro Leu Gly Pro Thr Val
             20             25             30
Pro Pro Gln Pro Pro Ser Ala Leu Glu Ser Asp Gly Glu Gly Pro Pro
             35             40             45
Pro Arg Val Gly Phe Val Asp Ser Thr Ile Lys Ser Leu Asp Lys Leu
             50             55             60
Arg Thr Leu Leu Tyr Gln Glu His Val Pro Thr Ser Ser Ala Ser Ala
             65             70             75             80
Gly Thr Pro Val Glu Val Gly Asp Arg Phe Thr Leu Glu Pro Leu Arg
  
```



```
<210> 588
<211> 707
<212> DNA
<213> Homo Sapiens
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-317-

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aagaattcac	ngtccgagat	ggctacatcc	attatggaca	aacagtc		707

&lt;210&gt; 589

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 589

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ttttgttaac	tttttgccac	actcaagtca	gtttaagtcc	tagcaaaaag	acggtagtta	180
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ggantnaaaa	t					551

&lt;210&gt; 590

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 590

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&lt;210&gt; 591

&lt;211&gt; 707

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 591

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<210> 592  
 <211> 541  
 <212> DNA  
 <213> Homo Sapiens

<400> 592  
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 cccccccctn ttngtttttn atccnttagg gggcacctgn cttnantngg cncaaaggat 180  
 ngccccctgt gcantgcaat ttggccnccg ccttggtcct gggttntagg taaaggtaag 240  
 gcnggtgnaa taantaatcc caccattncg naccaaattt actgnaacct gaacnggttg 300  
 ccgnacccan cncancctn cncgaaatgc aaaantttct ggnacaacnc aaacntacn 360  
 cncnccaccc ctntnctat ttncagctnc tacntcccca aaccacacnc ntaaattngn 420  
 attaaaatcc tntcctgtaa ttccaagcat ggctacttcc ccaccgccat tcaactnaag 480  
 gccnctacc acaggcncag nattaantgg ggcaaggaaa gggcccatcc ccccataaaa 540  
 t 541

<210> 593  
 <211> 605  
 <212> DNA  
 <213> Homo Sapiens

<400> 593  
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 ttttggttaac ttttgccac actcaantca gtttaantcc tagcaaaaaa acggtagtta 180  
 ggataccact gtggctgtaa atgatgnac actgggtgaa tttgtgctgg cgtttgtgtn 240  
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 gattgctcct gctgactgc aatgtggccg cggccctggg tctggtgtgt aagtaaagg 360  
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 ttgncggacc atctcaacc ttctcggaat gcanaaatgt ctgggacaan acnnaacata 480  
 ctctctcnc acctggttca tantttcagc ttctacatcc cccaaaccac actcntaaat 540  
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 gaaag 605

<210> 594  
 <211> 666  
 <212> DNA  
 <213> Homo Sapiens

<400> 594  
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 aaggcctcta cacaggcaca ggaatgactg gggcaaggan agggcccatt ccctcataaa 660  
 atgtatactc tgccttatct gtgctaata ttgtccagga aacgccanca ttttaccacc 720  
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 cccttgatgc ncagtttgaa aatgatgaac gaattacacc cttggaatcn gccctgatga 360  
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<210> 598  
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 <212> DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 598

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ccattttcca	t					491

## &lt;210&gt; 599

## &lt;211&gt; 802

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 599

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## &lt;210&gt; 600

## &lt;211&gt; 523

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 600

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cctgggtccca	tcccaggggc	ccagcctcgg	atnactcttc	anaaacacng	ccttnntgct	480
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## &lt;210&gt; 601

## &lt;211&gt; 530

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 601

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tnncaatttt	naaccttgc	cctctntccc	actgggtnaa	ccctggccca	tccccatcc	420
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## &lt;210&gt; 602

## &lt;211&gt; 311

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 602

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ccccgcgag	gngccgcgc	tgtgctctgg	ggatctnctg	ntcnaggtca	acntgcntca	300
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## &lt;210&gt; 603

## &lt;211&gt; 289

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 603

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## &lt;210&gt; 604

## &lt;211&gt; 356

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 604

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## &lt;210&gt; 605

## &lt;211&gt; 290

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 605

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nnantcgact	nccaccaact	gtnnntcttc	cttcctttcc	cnangtcctt	anntaccncc	180
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ctctctctct	ctcacctctt	tctccccctc	ccttcacnct	cacnttgctt		290

&lt;210&gt; 606

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 606

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tgtttacata	gttctttggg	attttactgt	tcctaatttt	attctgaaac	tcaattttac	660
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&lt;210&gt; 607

&lt;211&gt; 687

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 607

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tatttaactt	tgttatgcac	agttgtt				687

&lt;210&gt; 608

&lt;211&gt; 994

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 608

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&lt;210&gt; 609

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 609

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aag						843

&lt;210&gt; 610

&lt;211&gt; 707

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 610

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&lt;210&gt; 611



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 <211> 621  
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 <213> Homo Sapiens

<400> 612  
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 <212> DNA  
 <213> Homo Sapiens

<400> 613  
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 <211> 714  
 <212> DNA  
 <213> Homo Sapiens

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 <211> 688  
 <212> DNA  
 <213> Homo Sapiens

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 <213> Homo Sapiens

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<210> 618  
 <211> 461  
 <212> DNA  
 <213> Homo Sapiens

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<210> 619  
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 <212> DNA  
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 <212> DNA  
 <213> Homo Sapiens

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 aagtgtatgt tttgttgctt gctttcaggt tttgtttact ggaaaaaaa aaaaatgcc 420  
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<210> 621  
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 <212> DNA  
 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 626

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 627

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&lt;210&gt; 628

&lt;211&gt; 675

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 628

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<400> 630

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&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 632

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&lt;211&gt; 734

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 633

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&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 634

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 638

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 641

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 643

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## &lt;211&gt; 1041

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 647

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## &lt;210&gt; 648

## &lt;211&gt; 810

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 648

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 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

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 <212> DNA  
 <213> Homo Sapiens

<400> 651						
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&lt;210&gt; 652

&lt;211&gt; 518

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 652

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caaaactnaa	tgggcantcc	tntggctttc	tncctttccc	anatncccaa	caaggctact	420
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&lt;210&gt; 653

&lt;211&gt; 490

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 653

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gcnaatcccc						490

&lt;210&gt; 654

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 654

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&lt;210&gt; 655

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 <213> Homo Sapiens

<400> 655

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<400> 656

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 <211> 958  
 <212> DNA  
 <213> Homo Sapiens

<400> 657

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 <212> DNA  
 <213> Homo Sapiens

<400> 659						
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 <211> 824  
 <212> DNA  
 <213> Homo Sapiens

<400> 660						
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&lt;210&gt; 661

&lt;211&gt; 399

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 661

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&lt;210&gt; 662

&lt;211&gt; 826

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 662

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&lt;210&gt; 663

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 663

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## &lt;400&gt; 666

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## &lt;211&gt; 592

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 667

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## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 668

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## &lt;211&gt; 661

## &lt;212&gt; DNA

## &lt;213&gt; Homo Sapiens

## &lt;400&gt; 669

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&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 670

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&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 671

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 673

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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 674

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&lt;210&gt; 675

&lt;211&gt; 1067

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 675

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&lt;210&gt; 676

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 676

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&lt;210&gt; 677

&lt;211&gt; 1362

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens



&lt;400&gt; 677

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&lt;210&gt; 678

&lt;211&gt; 1771

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 678

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&lt;210&gt; 679

&lt;211&gt; 1367

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 679

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&lt;210&gt; 680

&lt;211&gt; 2545

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 680

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&lt;210&gt; 681

&lt;211&gt; 1745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 681

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&lt;210&gt; 682

&lt;211&gt; 1745

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 682

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&lt;210&gt; 683

&lt;211&gt; 3127

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 683

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 <211> 803  
 <212> PRT  
 <213> Homo Sapiens

<400> 684  
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 35 40 45  
 Gln Val Ser Ala Asn Asn Gln Phe Ser Ile Thr Lys Asn Arg Asp Gly  
 50 55 60  
 Arg Glu Asn Arg Arg Arg Asn Ser Lys Ile Gly Asp Asp Asn Glu Asn  
 65 70 75 80  
 Leu Thr Phe Lys Leu Glu Val Asn Glu Leu Ser Gly Lys Leu Asp Asn  
 85 90 95  
 Thr Asn Glu Tyr Asn Ser Asn Asp Gly Lys Lys Leu Pro Gln Gly Glu  
 100 105 110  
 Ser Arg Ser Tyr Glu Val Met Gly Ser Met Glu Glu Thr Leu Cys Asn  
 115 120 125  
 Ile Asp Asp Arg Asp Gly Asn Arg Asn Val His Leu Glu Phe Thr Glu  
 130 135 140  
 Arg Glu Ser Arg Lys Asp Gly Glu Asp Glu Phe Val Lys Glu Met Arg  
 145 150 155 160  
 Glu Glu Arg Lys Phe Gln Lys Leu Lys Asn Lys Glu Glu Val Leu Lys  
 165 170 175  
 Ala Ser Arg Glu Lys Val Leu Met Asp Glu Gly Ala Val Leu Thr  
 180 185 190  
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 195 200 205  
 Ser Asn Val Phe Asn Ile Leu Arg Glu Asn Asp Phe Glu Pro Lys Phe  
 210 215 220  
 Leu Cys Glu Val Lys Leu Ala Phe Lys Cys Asp Gly Glu Ile Lys Thr  
 225 230 235 240  
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 Gln Gly Gly Arg Lys Tyr Gly Ile Gln Glu Lys Arg Asp Lys Thr Leu  
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 Ile Asp Ser Xaa His Arg Ala Gly Glu Ile Thr Ser Asp Gly Leu Ser  
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 305 310 315 320  
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 Glu Glu Ala Ser Gly Met Glu Asp Asp Glu Asp Thr Ser Gly Leu Glu  
 340 345 350  
 Glu Glu Glu Glu Glu Glu Ala Ser Gly Leu Glu Glu Asp Xaa Ser Ser  
 355 360 365  
 Xaa Leu Glu Glu Glu Glu Glu Gln Thr Ser Glu Gln Asp Ser Thr Phe  
 370 375 380  
 Xaa Gly His Thr Leu Val Asp Ala Lys His Glu Val Glu Ile Thr Ser

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Thr Ser Leu Thr Glu Lys Lys Ala Ser Arg Arg Gln Lys Glu Ile Pro						
	435			440		445
Phe Ser Tyr Leu Val Gly Asp Ser Gly Lys Lys Lys Leu Val Lys His						
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Gln Val Val His Lys Thr Gln Glu Glu Glu Glu Thr Ala Val Pro Thr						
	465			470		475
Ser Gln Gly Thr Gly Thr Thr Cys Leu Thr Leu Cys Leu Ala Ser Pro						
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Ser Lys Ser Leu Glu Met Ser His Asp Glu His Lys Lys His Ser His						
	500			505		510
Thr Asn Leu Ser Ile Ser Thr Gly Val Thr Lys Leu Lys Lys Thr Glu						
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Glu Lys Lys His Arg Thr Leu His Thr Glu Glu Leu Thr Ser Lys Glu						
	530			535		540
Ala Asp Leu Thr Glu Glu Thr Glu Glu Asn Leu Arg Ser Ser Val Ile						
	545			550		555
Asn Ser Ile Arg Glu Ile Lys Glu Glu Ile Gly Asn Leu Lys Ser Ser						
	565			570		575
His Ser Gly Val Leu Glu Ile Glu Asn Ser Val Asp Asp Leu Ser Ser						
	580			585		590
Arg Met Asp Ile Leu Glu Glu Arg Ile Asp Ser Leu Glu Asp Gln Ile						
	595			600		605
Glu Glu Phe Ser Lys Asp Thr Met Gln Met Thr Lys Gln Ile Ile Ser						
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Lys Glu Gly Pro Arg Asp Ile Glu Glu Arg Ser Arg Ser Cys Asn Ile						
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Arg Leu Ile Gly Ile Pro Glu Lys Glu Ser Tyr Glu Asn Arg Ala Glu						
	645			650		655
Asp Ile Ile Lys Glu Ile Ile Asp Glu Asn Phe Ala Glu Leu Lys Lys						
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Gly Ser Ser Leu Glu Ile Val Ser Ala Cys Arg Val Pro Ser Lys Ile						
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Ser Ser Asp Lys Glu Lys Ile Ile Arg Pro Ser Arg Glu Arg Arg Glu						
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Leu Glu Lys Gly Phe Asn Pro Arg Thr Leu Tyr Pro Ala Lys Met Ala						
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Phe Asp Phe Arg Gly Lys Thr Lys Val Phe Leu Ser Ile Glu Glu Phe						
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Arg Asp Tyr Val Leu His Met Pro Thr Leu Arg Glu Leu Leu Gly Asn						
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Asn Ile Pro						800

&lt;210&gt; 685

&lt;211&gt; 947

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 685

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Gln Tyr Leu Gln Lys Val Val Leu Lys Asp Leu Trp Lys His Ser Phe
35      40      45
Ser Trp Pro Phe Gln Arg Pro Val Asp Ala Val Lys Leu Lys Leu Pro
50      55      60
Asp Tyr Tyr Thr Ile Ile Lys Asn Pro Met Asp Leu Asn Thr Ile Lys
65      70      75      80
Lys Arg Leu Glu Asn Lys Tyr Tyr Ala Lys Ala Ser Glu Cys Ile Glu
85      90      95
Asp Phe Asn Thr Met Phe Ser Asn Cys Tyr Leu Tyr Asn Lys Pro Gly
100     105     110
Asp Asp Ile Val Leu Met Ala Gln Ala Leu Glu Lys Leu Phe Met Gln
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Lys Leu Ser Gln Met Pro Gln Glu Glu Gln Val Val Gly Val Lys Glu
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Arg Ile Lys Lys Gly Thr Gln Gln Asn Ile Ala Val Ser Ser Ala Lys
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Glu Lys Ser Ser Pro Ser Ala Thr Glu Lys Val Phe Lys Gln Gln Glu
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Ile Pro Ser Val Phe Pro Lys Thr Ser Ile Ser Pro Leu Asn Val Val
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Gln Gly Ala Ser Val Asn Ser Ser Ser Gln Thr Ala Ala Gln Val Thr
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Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr Pro Ala Thr Ser Ala
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Val Lys Ala Ser Ser Glu Phe Ser Pro Thr Phe Thr Glu Lys Ser Val
225     230     235     240
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Phe Ala Ala Asp Val Arg Leu Met Phe Met Asn Cys Tyr Lys Tyr Asn
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Pro Pro Asp His Glu Val Val Thr Met Ala Arg Met Leu Gln Asp Val
355     360     365
Phe Glu Thr His Phe Ser Lys Ile Pro Ile Glu Pro Val Glu Ser Met
370     375     380
Pro Leu Cys Tyr Ile Lys Thr Asp Ile Thr Glu Thr Thr Gly Arg Glu
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 Asn Lys Lys Lys Glu Lys Ser Lys Lys Glu Lys Lys Lys Glu Lys Val  
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 485 490 495  
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 Lys Arg Pro Leu Lys Pro Pro Ala Lys Lys Ile Met Met Ser Lys Glu  
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&lt;210&gt; 686

&lt;211&gt; 3106

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 686

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aaaatgcata	tggtaaaatg	attgctttca	gataacaaga	taccaatctt	atattgtatt	3060
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&lt;210&gt; 687

&lt;211&gt; 1759

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 687

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1759

<210> 688  
 <211> 207  
 <212> PRT  
 <213> Homo Sapiens

<400> 688  
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 1 5 10 15  
 Met Glu Lys Leu Pro Thr Lys Lys Arg Gly Arg Lys Pro Ala Gly Leu  
 20 25 30  
 Ile Ser Ala Ser Arg Lys Val Pro Asn Leu Ser Val Ser Lys Leu Ile  
 35 40 45  
 Thr Glu Ala Leu Ser Val Ser Gln Glu Arg Val Gly Met Ser Leu Val  
 50 55 60  
 Ala Leu Lys Lys Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys Asn  
 65 70 75 80  
 Asn Ser Arg Ile Lys Leu Ser Leu Lys Ser Leu Val Asn Lys Gly Ile  
 85 90 95  
 Leu Val Gln Thr Arg Gly Thr Gly Ala Ser Gly Ser Phe Lys Leu Ser  
 100 105 110  
 Lys Lys Val Ile Pro Lys Ser Thr Arg Ser Lys Ala Lys Lys Ser Val  
 115 120 125  
 Ser Ala Lys Thr Lys Lys Leu Val Leu Ser Arg Asp Ser Lys Ser Pro  
 130 135 140  
 Lys Thr Ala Lys Thr Asn Lys Arg Ala Lys Lys Pro Arg Ala Thr Thr  
 145 150 155 160  
 Pro Lys Thr Val Arg Ser Gly Arg Lys Ala Lys Gly Ala Lys Gly Lys  
 165 170 175  
 Gln Gln Gln Lys Ser Pro Val Lys Ala Arg Ala Ser Lys Ser Lys Leu  
 180 185 190  
 Thr Gln His His Glu Val Asn Val Arg Lys Ala Thr Ser Lys Lys  
 195 200 205

<210> 689  
 <211> 1464  
 <212> DNA  
 <213> Homo Sapiens

<400> 689  
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 aaggaagaat ttctctgaa gcaccggaac ttgtactac cagcaccatg ccctaccaat 180  
 atccagcact gaccccgagg cagaagaagg agctgtctga catcgctcac cgcacgtgg 240  
 cacctggcaa gggcatcctg gctgcagatg agtccactgg gagcattgcc aagcggctgc 300  
 agtccattgg caccgagaac accgaggaga accggcgctt ctaccgccag ctgctgctga 360  
 cagctgacga ccgcgtgaac cctgcattg ggggtgtcat cctcttccat gagacactct 420  
 accagaaggc ggatgatggg cgtcccttcc cccaagttat caaatccaag ggcggtgttg 480  
 tgggcatcaa ggtagacaag ggcgtgggtcc ccctggcagg gacaaatggc gagactacca 540  
 cccaaggggt ggatgggctg tctgagcgct gtgcccagta caagaaggac ggagctgact 600  
 tcgccaagtg gcgttgtgtg ctgaagattg gggaacacac cccctcagcc ctgcacatca 660  
 tggaaaatgc caatgttctg gcccgttatg ccagtatctg ccagcagaat ggcattgtgc 720  
 ccacgtgga gcctgagatc ctccctgatg gggaccatga cttgaagcgc tgccagtatg 780  
 tgaccgagaa ggtgctggct gctgtctaca aggtctgag tgaccaccac atctacctgg 840

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tcactgggat caccttcttg tctggaggcc agagtgagga ggaggcgctc atcaacctca 1020
atgccattaa caagtgcccc ctgctgaagc cctggggcct gaccttctcc tacggccgag 1080
ccctgcaggc ctctgccctg aaggcctggg gcgggaagaa ggagaacctg aaggctgcgc 1140
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aagaggaggc cgctcctcgc gggctccagg ctggcttgcc cgcgctcttt cttccctcgt 1380
gacagtgggtg tgtgggtgctg tctgtgaatg ctaagtcacat caccctttcc ggcacactgc 1440
caaataaaca gctattttaag gggg 1464

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&lt;210&gt; 690

&lt;211&gt; 363

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 690

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Pro Tyr Gln Tyr Pro Ala Leu Thr Pro Glu Gln Lys Lys Glu Leu Ser
1      5      10      15
Asp Ile Ala His Arg Ile Val Ala Pro Gly Lys Gly Ile Leu Ala Ala
20     25     30
Asp Glu Ser Thr Gly Ser Ile Ala Lys Arg Leu Gln Ser Ile Gly Thr
35     40     45
Glu Asn Thr Glu Glu Asn Arg Arg Phe Tyr Arg Gln Leu Leu Leu Thr
50     55     60
Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe His
65     70     75     80
Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln Val
85     90     95
Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly Val
100    105    110
Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp
115    120    125
Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe
130    135    140
Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala
145    150    155    160
Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile
165    170    175
Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro
180    185    190
Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys Val
195    200    205
Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu Glu
210    215    220
Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys Thr
225    230    235    240
Gln Lys Phe Ser His Glu Glu Ile Ala Met Ala Thr Val Thr Ala Leu
245    250    255
Arg Arg Thr Val Pro Pro Ala Val Thr Gly Ile Thr Phe Leu Ser Gly
260    265    270
Gly Gln Ser Glu Glu Glu Ala Ser Ile Asn Leu Asn Ala Ile Asn Lys
275    280    285
Cys Pro Leu Leu Lys Pro Trp Ala Leu Thr Phe Ser Tyr Gly Arg Ala

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290                      295                      300  
 Leu Gln Ala Ser Ala Leu Lys Ala Trp Gly Gly Lys Lys Glu Asn Leu  
 305                      310                      315                      320  
 Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser Leu  
                          325                      330                      335  
 Ala Cys Gln Gly Lys Tyr Thr Pro Ser Gly Gln Ala Gly Ala Ala Ala  
                          340                      345                      350  
 Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr  
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<210> 691  
 <211> 1216  
 <212> DNA  
 <213> Homo Sapiens

<400> 691  
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 cacaacatct cagatgcttt tgaccagaag ttctcaaagg tgcctaccaa ggtcaaaggc 240  
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 gagttcttcg aggaggacaa catgctgagc atgggcaaga agatgatgca ggaggccatg 360  
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 gagacagaga ggctgatcca ggagctggcc aagtgcaga ttgacacaca caataaatt 780  
 gtcaaccagc tctgtcttccc cgaccccgag aagccctgca agatgtgtga ggcccgtcac 840  
 aagatccagg ccaagtatct ggaccagatg gaggacctgt atgaagactt ccacatcgtg 900  
 aagctgccgc tgttacccca tgaggtgctg ggggcagaca aggtcaacac cttctcgccc 960  
 ctctcctcgt agccctacaa gccccccagt gccagtagc acagctgcca gcccacaccg 1020  
 ctgccatttc acactacccc tccaccctcc ccacccctc ggggcagagt ttgcacaaag 1080  
 tcccccccat aatacagggg gagccacttg ggcaggaggg agggaggggt ccattccccc 1140  
 tgggtggggt ggtggggagc tgtagttgcc ccctacctct cccacctctt gctcttcaat 1200  
 aaatgatctt aaactg 1216

<210> 692  
 <211> 1958  
 <212> DNA  
 <213> Homo Sapiens

<400> 692  
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 tcccgccac gtccatttc gccctcgcg tccggagtcc ccgtggccag atctaaccat 180  
 gagctaccct ggctatcccc cgccccagg tggctaccca ccagctgcac caggtggtgg 240  
 tccctgggga ggtgctgctt accctcctcc gccagcatg ccccccacg ggctggataa 300  
 cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360  
 gtctgggaca tttggaggag ccaacatgcc caacctgtac cctggggccc ctggggctgg 420  
 ctaccacca gtgccccctg gcggttttgg gcagccccc tctgcccagc agcctgttcc 480  
 tccctatggg atgtatccac cccaggagg aaaccacccc tccaggatgc cctcatatcc 540  
 gccatacca ggggcccctg tgccgggcca gcccatgcca cccccggac agcagcccc 600  
 aggggcctac cctgggcagc caccagtgc ctacctggt cagcctccag tgccactccc 660

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ccccctgcga gatgccgagg tcttgccgaa ggccatgaaa ggcttcggga cggatgagca 840
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ttgctgctaa aatagatggt tcattttttct gaaaaaaaa 1958

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&lt;210&gt; 693

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 693

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Met Ser Tyr Pro Gly Tyr Pro Pro Pro Gly Gly Tyr Pro Pro Ala
1          5          10          15
Ala Pro Gly Gly Gly Pro Trp Gly Gly Ala Ala Tyr Pro Pro Pro Pro
20          25          30
Ser Met Pro Pro Ile Gly Leu Asp Asn Val Ala Thr Tyr Ala Gly Gln
35          40          45
Phe Asn Gln Asp Tyr Leu Ser Gly Met Ala Ala Asn Met Ser Gly Thr
50          55          60
Phe Gly Gly Ala Asn Met Pro Asn Leu Tyr Pro Gly Ala Pro Gly Ala
65          70          75          80
Gly Tyr Pro Pro Val Pro Pro Gly Gly Phe Gly Gln Pro Pro Ser Ala
85          90          95
Gln Gln Pro Val Pro Pro Tyr Gly Met Tyr Pro Pro Pro Gly Gly Asn
100         105         110
Pro Pro Ser Arg Met Pro Ser Tyr Pro Pro Tyr Pro Gly Ala Pro Val
115         120         125
Pro Gly Gln Pro Met Pro Pro Pro Gly Gln Gln Pro Pro Gly Ala Tyr
130         135         140
Pro Gly Gln Pro Pro Val Thr Tyr Pro Gly Gln Pro Pro Val Pro Leu
145         150         155         160
Pro Gly Gln Gln Gln Pro Val Pro Ser Tyr Pro Gly Tyr Pro Gly Ser
165         170         175
Gly Thr Val Thr Pro Ala Val Pro Pro Thr Gln Phe Gly Ser Arg Gly
180         185         190
Thr Ile Thr Asp Ala Pro Gly Phe Asp Pro Leu Arg Asp Ala Glu Val
195         200         205

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Leu Arg Lys Ala Met Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Ile  
 210 215 220  
 Asp Cys Leu Gly Ser Arg Ser Asn Lys Gln Arg Gln Gln Ile Leu Leu  
 225 230 235 240  
 Ser Phe Lys Thr Ala Tyr Gly Lys Asp Leu Ile Lys Asp Leu Lys Ser  
 245 250 255  
 Glu Leu Ser Gly Asn Phe Glu Lys Thr Ile Leu Ala Leu Met Lys Thr  
 260 265 270  
 Pro Val Leu Phe Asp Ile Tyr Glu Ile Lys Glu Ala Ile Lys Gly Val  
 275 280 285  
 Gly Thr Asp Glu Ala Cys Leu Ile Glu Ile Leu Ala Ser Arg Ser Asn  
 290 295 300  
 Glu His Ile Arg Glu Leu Asn Arg Ala Tyr Lys Ala Glu Phe Lys Lys  
 305 310 315 320  
 Thr Leu Glu Glu Ala Ile Arg Ser Asp Thr Ser Gly His Phe Gln Arg  
 325 330 335  
 Leu Leu Ile Ser Leu Ser Gln Gly Asn Arg Asp Glu Ser Thr Asn Val  
 340 345 350  
 Asp Met Ser Leu Ala Gln Arg Asp Ala Gln Glu Leu Tyr Ala Ala Gly  
 355 360 365  
 Glu Asn Arg Leu Gly Thr Asp Glu Ser Lys Phe Asn Ala Val Leu Cys  
 370 375 380  
 Ser Arg Ser Arg Ala His Leu Val Ala Val Phe Asn Glu Tyr Gln Arg  
 385 390 395 400  
 Met Thr Gly Arg Asp Ile Glu Lys Ser Ile Cys Arg Glu Met Ser Gly  
 405 410 415  
 Asp Leu Glu Glu Gly Met Leu Ala Val Lys Cys Leu Lys Asn Thr  
 420 425 430  
 Pro Ala Phe Ala Glu Arg Leu Asn Lys Ala Met Arg Gly Ala Gly  
 435 440 445  
 Thr Lys Asp Arg Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Thr  
 450 455 460  
 Asp Leu Leu Asp Ile Arg Ser Glu Tyr Lys Arg Met Tyr Gly Lys Ser  
 465 470 475 480  
 Leu Tyr His Asp Ile Ser Gly Asp Thr Ser Gly Asp Tyr Arg Lys Ile  
 485 490 495  
 Leu Leu Lys Ile Cys Gly Gly Asn Asp  
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<210> 694  
 <211> 1141  
 <212> DNA  
 <213> Homo Sapiens

<400> 694  
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 cctgatgggt ggaaggaacc agctttttcc aaagaggaca atcccagagg acttttggag 180  
 gagagcagtt tcgcaacttt gttcccaaaa tacagggaag cttacttgaa agagtgttgg 240  
 ccattggtgc agaaagcctt aaatgaacat catgttaatg caaccctgga cctgatcgaa 300  
 ggcagcatga ctgtttgtac tacaagaag acttttgatc catatatcat cattagggcc 360  
 agagatctga taaaactggt agcaaggagt gtttcatttg aacaggcagt acgaattctt 420  
 caggatgatg ttgcatgtga catcattaaa ataggttctt tagtaaggaa taaagagaga 480  
 tttgtaaaac gaagacaacg gcttattggt cccaaaggat ctacattgaa ggcattggaa 540  
 ctcttaacta attgttacat tatggttcag ggaaacacag tttcagccat tggacctttt 600



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tataacatta aaagcttaat gattaagaga gagttggcaa aagattctga attacgatca 720
caaagttggg agagattttt gccacagttc aaacacaaaa atgtgaataa acgcaaggaa 780
ccaaagaaaa aaactgttaa gaaagatata cgccattccc accaccacaa ccagaaagtc 840
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tgaaactaaa attgatgtgg ccagcatcaa ggaaaagggt aagaaaagcaa agaataagaa 1080
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a

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<210> 695  
 <211> 288  
 <212> PRT  
 <213> Homo Sapiens

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<400> 695
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Glu Phe Arg Asn Gln Lys Pro Lys Pro Glu Asn Gln Asp Glu Ser Glu
 20          25          30
Leu Leu Thr Val Pro Asp Gly Trp Lys Glu Pro Ala Phe Ser Lys Glu
 35          40          45
Asp Asn Pro Arg Gly Leu Leu Glu Glu Ser Ser Phe Ala Thr Leu Phe
 50          55          60
Pro Lys Tyr Arg Glu Ala Tyr Leu Lys Glu Cys Trp Pro Leu Val Gln
 65          70          75          80
Lys Ala Leu Asn Glu His His Val Asn Ala Thr Leu Asp Leu Ile Glu
 85          90          95
Gly Ser Met Thr Val Cys Thr Thr Lys Lys Thr Phe Asp Pro Tyr Ile
100          105          110
Ile Ile Arg Ala Arg Asp Leu Ile Lys Leu Leu Ala Arg Ser Val Ser
115          120          125
Phe Glu Gln Ala Val Arg Ile Leu Gln Asp Asp Val Ala Cys Asp Ile
130          135          140
Ile Lys Ile Gly Ser Leu Val Arg Asn Lys Glu Arg Phe Val Lys Arg
145          150          155          160
Arg Gln Arg Leu Ile Gly Pro Lys Gly Ser Thr Leu Lys Ala Leu Glu
165          170          175
Leu Leu Thr Asn Cys Tyr Ile Met Val Gln Gly Asn Thr Val Ser Ala
180          185          190
Ile Gly Pro Phe Ser Gly Leu Lys Glu Val Arg Lys Val Val Leu Asp
195          200          205
Thr Met Lys Asn Ile His Pro Ile Tyr Asn Ile Lys Ser Leu Met Ile
210          215          220
Lys Arg Glu Leu Ala Lys Asp Ser Glu Leu Arg Ser Gln Ser Trp Glu
225          230          235          240
Arg Phe Leu Pro Gln Phe Lys His Lys Asn Val Asn Lys Arg Lys Glu
245          250          255
Pro Lys Lys Lys Thr Val Lys Lys Asp Ile Arg His Ser His His His
260          265          270
Asn Gln Lys Val Arg Ser Ile Lys Asn Trp Leu Val Val Asn Thr Phe
275          280          285

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<210> 696

&lt;211&gt; 1008

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 696

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&lt;210&gt; 697

&lt;211&gt; 685

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 697

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&lt;210&gt; 698

&lt;211&gt; 1205

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 698

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&lt;210&gt; 699

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 699

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&lt;210&gt; 700

&lt;211&gt; 1967

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 700

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&lt;210&gt; 701

&lt;211&gt; 3423

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 701

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ttg						3423

&lt;210&gt; 702

&lt;211&gt; 1106

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 702

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&lt;210&gt; 703

&lt;211&gt; 1095

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 703

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&lt;210&gt; 704

&lt;211&gt; 1968

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 704

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&lt;210&gt; 705

&lt;211&gt; 800

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 705

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&lt;210&gt; 706

&lt;211&gt; 487

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 706

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&lt;211&gt; 3599

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 707

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&lt;210&gt; 708

&lt;211&gt; 1123

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 708

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35          40          45
Gly Arg Asp Ser Leu Pro Phe Asp Phe Gln Gly His Ser Gly Pro Pro
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Phe Ala Asn Val Glu Glu His Ser Phe Ser Tyr Gly Ala Arg Asp Gly
65          70          75          80
Pro His Gly Asp Tyr Arg Gly Gly Glu Gly Pro Gly His Asp Phe Arg
85          90          95
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Leu Asp Phe Arg Gly Arg Asp Ile His Ser Gly Asp Phe Arg Asp Arg
115         120         125
Glu Gly Pro Pro Met Asp Tyr Arg Gly Gly Asp Gly Thr Ser Met Asp
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Tyr Arg Gly Arg Glu Ala Pro His Met Asn Tyr Arg Asp Arg Asp Ala
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His Ala Val Asp Phe Arg Gly Arg Asp Ala Pro Pro Ser Asp Phe Arg
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Gly Arg Gly Thr Tyr Asp Leu Asp Phe Arg Gly Arg Asp Gly Ser His
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Ala Asp Phe Arg Gly Arg Asp Leu Ser Asp Leu Asp Phe Arg Ala Arg
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 <212> DNA  
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<400> 709

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&lt;400&gt; 713

Asn Val Glu Glu Xaa His Ser Phe Ser Tyr

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10

&lt;210&gt; 714

&lt;211&gt; 10

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&lt;400&gt; 714

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&lt;211&gt; 10

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 715

Asp Thr Asp Tyr Xaa Arg Ser Met Glu Tyr  
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&lt;210&gt; 716

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 716

Ser Leu Leu Glu Xaa Asp Ala Ile Gly Cys  
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&lt;210&gt; 717

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 717

Thr Leu Met Ile Xaa Gln Asp Lys Glu Val  
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&lt;210&gt; 718

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&lt;213&gt; Homo Sapiens

&lt;400&gt; 718

Tyr Val Ser Ser Leu Asp Phe Trp Tyr Cys  
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&lt;210&gt; 719

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&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 719

Val Ile Val Glu Val Leu Glu Pro Tyr Val  
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&lt;211&gt; 10

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&lt;400&gt; 720

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Asn Val Glu Glu Xaa His Ser Phe Ser Tyr  
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Trp Gln Ser Ala Xaa Arg Phe Tyr Tyr Leu  
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&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 758

Ser Leu Leu Glu Xaa Asp Ala Ile Gly Cys  
1 5 10

&lt;210&gt; 759

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 759

Thr Leu Met Ile Xaa Gln Asp Lys Glu Val  
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&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 760

Tyr Val Ser Ser Leu Asp Phe Trp Tyr Cys  
1 5 10

&lt;210&gt; 761

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 761

Val Ile Val Glu Val Leu Glu Pro Tyr Val  
1 5 10

&lt;210&gt; 762

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 762

Lys Leu Thr Asp Xaa Trp Asn Lys Leu Ala  
1 5 10

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&lt;211&gt; 10

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&lt;400&gt; 763

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&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 789

Glu	Glu	Gln	Ser	Ser	Asp	Ala	Gly	Leu	Phe
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&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 790

Lys	Glu	Tyr	Asn	Xaa	Thr	Gly	Tyr	Asp	Tyr
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&lt;210&gt; 791

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 791

Thr	Glu	Ala	Lys	Gln	Glu	Leu	Ile	Thr	Tyr
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&lt;210&gt; 792

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 792

Val	Glu	Ala	Leu	Arg	Val	Val	Lys	Ile	Leu
1				5					10

&lt;210&gt; 793

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 793

Gly	Glu	Tyr	Gly	Xaa	Gly	Asp	Ser	Asp	Tyr
1				5					10

&lt;210&gt; 794

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 794

Leu Glu Arg Arg Glu Arg Glu Gly Lys Phe  
 1 5 10

&lt;210&gt; 795

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 795

Arg Gln Asp Gly Glu Ser Lys Thr Ile Met  
 1 5 10

&lt;210&gt; 796

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 796

Thr Pro Pro Glu Val Ile Val Glu Val Leu  
 1 5 10

&lt;210&gt; 797

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 797

Tyr Gly Phe Ile Asp Leu Asp Ser His Val  
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&lt;210&gt; 798

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 798

Arg Gln Phe Pro Xaa Asn Lys Glu Val Leu  
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&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 799

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&lt;210&gt; 800

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 800

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35 40 45
Thr Glu Asn Thr Glu Glu Asn Arg Arg Phe Tyr Arg Gln Leu Leu Leu
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Thr Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe
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His Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln
85 90 95
Val Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly
100 105 110
Val Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu
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Asp Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp
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Phe Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser
145 150 155 160
Ala Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser
165 170 175
Ile Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu
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Pro Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys
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Glu Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys
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 290 295 300  
 Ala Leu Gln Ala Ser Ala Leu Lys Ala Trp Gly Gly Lys Lys Glu Asn  
 305 310 315 320  
 Leu Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser  
 325 330 335  
 Leu Ala Cys Gln Gly Lys Tyr Thr Pro Ser Gly Gln Ala Gly Ala Ala  
 340 345 350  
 Ala Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr  
 355 360

&lt;210&gt; 801

&lt;211&gt; 3504

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 801

ctctgctttt ctctttcaga gctgttgccg agccattggt acctgtattg gggaaacata 60  
 gcatacaagc aagaagctta cagcctcagt ggcgaaaaat ttttcatgtc agagaccgag 120  
 aactcttgca gtcgttttat tcatcccttc ttctccagac agaagatacc aaaaagtgtc 180  
 aatcaaagat ctgttcatct tattgataaa gtcactaata agccaaaatg tctgtcaaag 240  
 tcaaccgcag cgtgtcagac cagtctctatc gctacaagat gccccggttg attgctaagg 300  
 ttgagggcaa aggaaatgga atcaagacag ttatagtcaa catgggtgac gttgcaaagg 360  
 cgcttaatcg gcctccaacg tatcccacca aatatttttg ttgtgagctg ggagcacaga 420  
 cccagtttga tgtaagaat gaccgttaca ttgtcaatgg atctcatgag gcgaataagc 480  
 tgcaagacat gttggatgga ttcattaaaa aatttgttct ctgtcctgag tgtgagaatc 540  
 ctgaaacaga tctgcatgtc aatccaaaga agcaaaacat aggtaatctt tgtaaagcct 600  
 gtgggtaccg aggcattgctt gacacacatc ataaactctg tacattcatt ctcaaaaacc 660  
 cacctgagaa tagtgacatt ggtacaggaa agaaagagaa agaaaagaaa aatagaaagg 720  
 gcaaggacaa ggaaaatggc tctgtatcca ccagtgtgac accaccacct ccaccaccaa 780  
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 agaagataag agagcaaadc aagaaatata ggcgccattt tttaagattt tgtcataaca 1140  
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 ctcagttgat ctccaagatt ccacatatct tgaaggagat gtatgatgca gaccttttag 1260  
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 aaagatttga ttttggatct tcttcagact ttgggctatg aatggcttat gctgaagtaa 1860  
 ttggctactt ttaggatggt acaccattta ataacttaga cttcttaagt ttggtagatt 1920

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gttaggtact gaagacttga agaattgcaaa caattataat gaccttactc agccattaag 1980
aatgaagta ttttgaaagt tgtgtctcca gtccattgag attggcaact gacaattctt 2040
gtcattctaa ggaaatttga tgatttaatg acagtgtgac atcctcatga gaagtaaaaa 2100
tgacctgtgt gtcctatggt ttaagagcaa attttgaaac ttggagtgtt ggtttttcag 2160
tttgtgtaca ctcaccccaa attgtagtct attgagtcac gtgcattgca cgttggataa 2220
gccagggaaa tgacaaataa gtattttgtg tgtatttagt gggtgctttg tactgagaga 2280
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taaaatcata ccaaacattt ggtaaaatta aaaccttgat gggaggctgg gcgtggaaca 3060
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aatttcccc tcctttcata ttaa 3504

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&lt;210&gt; 802

&lt;211&gt; 429

&lt;212&gt; PRT

&lt;213&gt; Homo. Sapiens

&lt;400&gt; 802

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Met Ser Val Asn Val Asn Arg Ser Val Ser Asp Gln Phe Tyr Arg Tyr
1 5 10 15
Lys Met Pro Arg Leu Ile Ala Lys Val Glu Gly Lys Gly Asn Gly Ile
20 25 30
Lys Thr Val Ile Val Asn Met Val Asp Val Ala Lys Ala Leu Asn Arg
35 40 45
Pro Pro Thr Tyr Pro Thr Lys Tyr Phe Gly Cys Glu Leu Gly Ala Gln
50 55 60
Thr Gln Phe Asp Val Lys Asn Asp Arg Tyr Ile Val Asn Gly Ser His
65 70 75 80
Glu Ala Asn Lys Leu Gln Asp Met Leu Asp Gly Phe Ile Lys Lys Phe
85 90 95
Val Leu Cys Pro Glu Cys Glu Asn Pro Glu Thr Asp Leu His Val Asn
100 105 110
Pro Lys Lys Gln Thr Ile Gly Asn Ser Cys Lys Ala Cys Gly Tyr Arg
115 120 125
Gly Met Leu Asp Thr His His Lys Leu Cys Thr Phe Ile Leu Lys Asn
130 135 140
Pro Pro Glu Asn Ser Asp Ile Gly Thr Gly Lys Lys Glu Lys Glu Lys
145 150 155 160
Lys Asn Arg Lys Gly Lys Asp Lys Glu Asn Gly Ser Val Ser Thr Ser

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165 170 175  
 Glu Thr Pro Pro Pro Pro Pro Asn Glu Ile Ser Pro Pro His Ala  
 180 185 190  
 Val Glu Glu Glu Glu Asp Asp Asp Trp Gly Glu Asp Thr Thr Glu Glu  
 195 200 205  
 Ala Gln Arg Arg Arg Met Asp Glu Ile Ser Asp His Ala Lys Gly Leu  
 210 215 220  
 Thr Leu Ser Asp Asp Leu Glu Arg Thr Val Glu Glu Arg Val Asn Ile  
 225 230 235 240  
 Leu Phe Asp Phe Val Lys Lys Lys Lys Glu Glu Gly Ile Ile Asp Ser  
 245 250 255  
 Ser Asp Lys Asp Ile Val Ala Glu Ala Glu Arg Leu Asp Val Lys Ala  
 260 265 270  
 Met Gly Pro Leu Val Leu Thr Glu Val Leu Phe Asp Glu Lys Ile Arg  
 275 280 285  
 Glu Gln Ile Lys Lys Tyr Arg Arg His Phe Leu Arg Phe Cys His Asn  
 290 295 300  
 Asn Lys Lys Ala Gln Arg Tyr Leu Leu His Gly Leu Glu Cys Val Val  
 305 310 315 320  
 Ala Met His Gln Ala Gln Leu Ile Ser Lys Ile Pro His Ile Leu Lys  
 325 330 335  
 Glu Met Tyr Asp Ala Asp Leu Leu Glu Glu Glu Val Ile Ile Ser Trp  
 340 345 350  
 Ser Glu Lys Ala Ser Lys Lys Tyr Val Ser Lys Glu Leu Ala Lys Glu  
 355 360 365  
 Ile Arg Val Lys Ala Glu Pro Phe Ile Lys Trp Leu Lys Glu Ala Glu  
 370 375 380  
 Glu Glu Ser Ser Gly Gly Glu Glu Glu Asp Glu Asp Glu Asn Ile Glu  
 385 390 395 400  
 Val Val Tyr Ser Lys Thr Ala Ser Val Pro Lys Val Glu Thr Val Lys  
 405 410 415  
 Ser Asp Asn Lys Asp Asp Asp Ile Asp Ile Asp Ala Ile  
 420 425

&lt;210&gt; 803

&lt;211&gt; 2251

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 803

aggatgtctt ctggcaattt catataagta ttttttcaaa aatgtctctt ctgtcaaccc 60  
 cagcctttg gcacaatgaa gtgggtaacc tttatttccc ttctttttct ctttagctcg 120  
 gcttattcca ggggtgtgtt tcgtcgagat gcacacaaga gtgagggtgc tcatcggttt 180  
 aaagatttgg gagaagaaaa tttcaaagcc ttggtgttga ttgcctttgc tcagtatctt 240  
 cagcagtgtc catttgaaga tcatgtaaaa ttagtgaatg aagtaactga atttgcaaaa 300  
 acatgtgtag ctgatgagtc agctgaaaat tgtgacaaat cacttcatac ccttttttga 360  
 gacaaattat gcacagttgc aactcttcgt gaaacctatg gtgaaatggc tgactgctgt 420  
 gcaaaacaag aacctgagag aaatgaatgc ttcttgcaac acaaagatga caaccctaac 480  
 ctccccgat tgggtgagac agagggtgat gtgatgtgca ctgcttttca tgacaatgaa 540  
 gagacatttt tgaaaaaata cttatatgaa attgccagaa gacatcctta cttttatgcc 600  
 ccggaactcc ttttctttgc taaaaggat aaagctgctt ttacagaatg ttgccaagct 660  
 gctgataaag ctgcctgcct gttgccaag ctcgatgaac ttcgggatga agggaaggct 720  
 tcgtctgcca aacagagact caaatgtgcc agtctccaaa aatttggaga aagagctttc 780  
 aaagcatggg cagtggctcg cctgagccag agatttccca aagctgagtt tgcagaagtt 840  
 tccaagttag tgacagatct taccaaagtc cacacggaat gctgccaatg agatctgctt 900

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gaatgtgctg atgacagggc ggaccttgcc aagtatatct gtgaaaatca ggattcgatc 960
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tatctatccg tggctctgaa ccagttatgt gtgttgcatg agaaaacgcc agtaagtgc 1560
agagtcacaa aatgtgcac agagtccttg gtgaacaggc gaccatgctt ttcagctctg 1620
agagtcgatg aaacatacgt tcccaaagag tttaatgtcg aaacattcac cttccatgca 1680
gatatatgca cactttctga gaaggagaga caaatcaaga aacaaactgc acttggtgag 1740
cttggtgaaac acaagcccaa ggcaacaaaa gagcaactga aagctgttat ggatgatttc 1800
gcagcttttg tagagaagtg ctgcaaggct gacgataagg agacctgctt tgcgaggag 1860
ggtaaaaaaac ttgttgctgc aagtcaagct gccttaggct tataacatct acatttaaaa 1920
gcctctcagc ctaccatgag aataagagaa agaaaatgaa gatcaaaagc ttattcatct 1980
gttttctttt tcgttggtgt aaagccaaca ccctgtctaa aaaacataaa tttctttaat 2040
cattttgcct cttttctctg tgcttcaatt aataaaaaat ggaaagaatc taatagagtg 2100
gtacagcact gttatttttc aaagatgtgt tgctatcctg aaaattctgt aggttctgtg 2160
gaagttccag tgttctctct tattccactt cggtagagga tttctagttt ctgtgggcta 2220
attaaataaa tcactaatac tcttctaagt t 2251

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&lt;210&gt; 804

&lt;211&gt; 609

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 804

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Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1           5           10          15
Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
20          25          30
His Arg Phe Lys Asp Leu Gly Glu Asn Phe Lys Ala Leu Val Leu
35          40          45
Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50          55          60
Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65          70          75          80
Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85          90          95
Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100         105         110
Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115         120         125
His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130         135         140
Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145         150         155         160
Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165         170         175
Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180         185         190
Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu

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195	200	205
Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys		
210	215	220
Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val		
225	230	235
Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser		
245	250	255
Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly		
260	265	270
Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile		
275	280	285
Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu		
290	295	300
Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp		
305	310	315
Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser		
325	330	335
Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly		
340	345	350
Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val		
355	360	365
Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys		
370	375	380
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu		
385	390	395
Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys		
405	410	415
Glu Leu Phe Lys Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu		
420	425	430
Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val		
435	440	445
Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His		
450	455	460
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val		
465	470	475
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg		
485	490	495
Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe		
500	505	510
Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala		
515	520	525
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu		
530	535	540
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys		
545	550	555
Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala		
565	570	575
Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe		
580	585	590
Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly		
595	600	605
Leu		

&lt;210&gt; 805

&lt;211&gt; 1356

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 805

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acaaacacca aggagtggag gtcagagtgt cacttttttg ttttcttttt gaaagatcat    60
tcgagaaaca cgtcactgat ctcccctgcg accatgtctt ccattaagat tgagtgtggt    120
ttgccagaga actgccgggtg tgggtgagtct ccagtatggg aggaagtgtc caactctctg    180
ctctttgtag acattcctgc aaaaaagggt tgccgggtggg attcattcac caagcaagta    240
cagcgagtga ccatggatgc cccagtcagc tccgtggctc ttcgccagtc gggaggctat    300
gttgccacca ttggaacaaa gttctgtgct ttgaactgga aagaacaatc agcagttgtc    360
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gccgggaggt actttgctgg caccatggct gaggaacacg ctccagcagt tcttgagcgg    480
caccaggggg ccctgtactc cctctttcct gatcaccacg tgaaaaagta ctttgaccag    540
gtggacattt ccaatgggtt ggattggctg ctagaccaca aaatcttcta ttacattgac    600
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cgcagaagtg tttacaagct agaaaaggaa gaacaaatcc cagatggaat gtgtattgat    720
gctgagggga agctctgggt ggcctgttac aatggaggaa gagtgattcg tttagatcct    780
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gaggtctctt tgaggcaacc tgaagctggg ggaattttca agataactgg tctgggggtc    960
aaaggaattg ctccctactc ctatgcggga tgaggacagg tcttctttcc tgccagaggg   1020
agctctgaag acaactagag aattctgggc ctgaaatttc aatctagtta gaaagaaaaa   1080
tgaggcaatg attttattaa cagcgtaag ttttaattta caacttttaa aaggcagagc   1140
atttttaaca aggggtgaca ggtgggtttg ataacacact tataaggctt tctgtaaaag   1200
gtactataga agggcgaaga atcgttcaac tgtcaatcag cctcttgatt ctttgtaaat   1260
tgccaggggt ggtgggtaca tatctcttct tgattctgca tttcatactt aactatatta   1320
aagcttcaag gaacaataaa tagtaacctg gtaatg                                1356

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&lt;210&gt; 806

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 806

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Met Ser Ser Ile Lys Ile Glu Cys Val Leu Pro Glu Asn Cys Arg Cys
 1           5           10           15
Gly Glu Ser Pro Val Trp Glu Glu Val Ser Asn Ser Leu Leu Phe Val
 20           25           30
Asp Ile Pro Ala Lys Lys Val Cys Arg Trp Asp Ser Phe Thr Lys Gln
 35           40           45
Val Gln Arg Val Thr Met Asp Ala Pro Val Ser Ser Val Ala Leu Arg
 50           55           60
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
 65           70           75           80
Asn Trp Lys Glu Gln Ser Ala Val Val Leu Ala Thr Val Asp Asn Asp
 85           90           95
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
100           105           110
Tyr Phe Ala Gly Thr Met Ala Glu Thr Ala Pro Ala Val Leu Glu
115           120           125
Arg His Gln Gly Ala Leu Tyr Ser Leu Phe Pro Asp His His Val Lys
130           135           140
Lys Tyr Phe Asp Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
145           150           155           160

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Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Ser Val Asp  
 165 170 175  
 Ala Phe Asp Tyr Asp Leu Gln Thr Gly Gln Ile Ser Asn Arg Arg Ser  
 180 185 190  
 Val Tyr Lys Leu Glu Lys Glu Glu Gln Ile Pro Asp Gly Met Cys Ile  
 195 200 205  
 Asp Ala Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val  
 210 215 220  
 Ile Arg Leu Asp Pro Val Thr Gly Lys Arg Leu Gln Thr Val Lys Leu  
 225 230 235 240  
 Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asn Tyr Ser  
 245 250 255  
 Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Asp Pro Glu Gly Leu  
 260 265 270  
 Leu Arg Gln Pro Glu Ala Gly Gly Ile Phe Lys Ile Thr Gly Leu Gly  
 275 280 285  
 Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly  
 290 295

&lt;210&gt; 807

&lt;211&gt; 1980

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 807

atgccaaagta	gtttgctgct	agcaaccaga	aaccaaattcc	tgtctatgat	gaactggttg	60
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atgaaagccg	cggagagggg	agatgtagaa	aaagtttctt	caatccttgc	taaaaagggc	180
atcaatccag	gcaaactaga	tgtggaaggc	agatctgcct	tccatggtgt	ggcctcaaag	240
gggaatcttg	aatgtttgaa	tgccatcctt	atacatggag	ttgatattac	aaccagtgc	300
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atattactgg	ataaagtcaa	tggtttacaa	ctacagctga	atgaggaagt	gatggttgct	1020
gatgatctgg	aaagtgcaga	agaaaagctg	aagtcctctt	tgggtggctaa	agaaaagcaa	1080
catgaagaaa	gcctaagaac	tattgagtct	ctgaaaaaca	gatttaaata	ttttgagtgt	1140
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tcattaccca	atcaaacctc	atattctgaa	aatgacctct	taaagaaaga	gttagaagca	1260
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&lt;210&gt; 808

&lt;211&gt; 659

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 808

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 Trp Asn Lys Tyr Asp Asp Arg Leu Met Lys Ala Ala Glu Arg Gly Asp  
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 Val Glu Lys Val Ser Ser Ile Leu Ala Lys Lys Gly Ile Asn Pro Gly  
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 Lys Leu Asp Val Glu Gly Arg Ser Ala Phe His Val Val Ala Ser Lys  
 65 70 75 80  
 Gly Asn Leu Glu Cys Leu Asn Ala Ile Leu Ile His Gly Val Asp Ile  
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 Thr Thr Ser Asp Thr Ala Gly Arg Asn Ala Leu His Leu Ala Ala Lys  
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 Tyr Gly His Ala Leu Cys Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro  
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&lt;210&gt; 809

&lt;211&gt; 1725

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 809

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&lt;210&gt; 810

&lt;211&gt; 355

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 810

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Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
35          40          45
Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
50          55          60
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65          70          75          80
Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85          90          95
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115         120         125
His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130         135         140
Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser
145         150         155         160
Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly
165         170         175
Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
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195         200         205
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
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 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln  
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 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala  
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 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu  
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 Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His  
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 Val Gln Thr  
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 <212> DNA  
 <213> Homo Sapiens

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 <212> PRT  
 <213> Homo Sapiens

<400> 812  
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50	55	60
Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys		
65	70	75
Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Glu Ala		
85	90	95
Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn		
100	105	110
Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys		
115	120	125
Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr		
130	135	140
Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys		
145	150	155
Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr		
165	170	175
Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly		
180	185	190
Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly		
195	200	205
Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu		
210	215	220
Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr		
225	230	235
Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr		
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Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe		
260	265	270
Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu		
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 <211> 5175  
 <212> DNA  
 <213> Homo Sapiens

<400> 813

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tatgtatata ttttttaaaa atctatatatt tgggaaaaaa acatacacia tgtgtctttc 5100
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<210> 814  
 <211> 1392  
 <212> PRT  
 <213> Homo Sapiens

<400> 814

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Met Ser Met Leu Lys Pro Ser Gly Leu Lys Ala Pro Thr Lys Ile Leu
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Lys Pro Gly Ser Thr Ala Leu Lys Thr Pro Thr Ala Val Val Ala Pro
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Val Glu Lys Thr Ile Ser Ser Glu Lys Ala Ser Ser Thr Pro Ser Ser
35          40          45
Glu Thr Gln Glu Glu Phe Val Asp Asp Phe Arg Val Gly Glu Arg Val
50          55          60
Trp Val Asn Gly Asn Lys Pro Gly Phe Ile Gln Phe Leu Gly Glu Thr
65          70          75          80
Gln Phe Ala Pro Gly Gln Trp Ala Gly Ile Val Leu Asp Glu Pro Ile
85          90          95
Gly Lys Asn Asp Gly Ser Val Ala Gly Val Arg Tyr Phe Gln Cys Glu
100         105         110
Pro Leu Lys Gly Ile Phe Thr Arg Pro Ser Lys Leu Thr Arg Lys Val
115         120         125
Gln Ala Glu Asp Glu Ala Asn Gly Leu Gln Thr Thr Pro Ala Ser Arg
130         135         140
Ala Thr Ser Pro Leu Cys Thr Ser Thr Ala Ser Met Val Ser Ser Ser
145         150         155         160
Pro Ser Thr Pro Ser Asn Ile Pro Gln Lys Pro Ser Gln Pro Ala Ala
165         170         175
Lys Glu Pro Ser Ala Thr Pro Pro Ile Ser Asn Leu Thr Lys Thr Ala
180         185         190
Ser Glu Ser Ile Ser Asn Leu Ser Glu Ala Gly Ser Ile Lys Lys Gly
195         200         205
Glu Arg Glu Leu Lys Ile Gly Asp Arg Val Leu Val Gly Gly Thr Lys

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Ala Gly Val Val Arg Phe Leu Gly Glu Thr Asp Phe Ala Lys Gly Glu		
225	230	235
Trp Cys Gly Val Glu Leu Asp Glu Pro Leu Gly Lys Asn Asp Gly Ala		240
	245	250
Val Ala Gly Thr Arg Tyr Phe Gln Cys Gln Pro Lys Tyr Gly Leu Phe		255
	260	265
Ala Pro Val His Lys Val Thr Lys Ile Gly Phe Pro Ser Thr Thr Pro		270
	275	280
Ala Lys Ala Lys Ala Asn Ala Val Arg Arg Val Met Ala Thr Thr Ser		285
	290	295
Ala Ser Leu Lys Arg Ser Pro Ser Ala Ser Ser Leu Ser Ser Met Ser		300
305	310	315
Ser Val Ala Ser Ser Val Ser Ser Arg Pro Ser Arg Thr Gly Leu Leu		320
	325	330
Thr Glu Thr Ser Ser Arg Tyr Ala Arg Lys Ile Ser Gly Thr Thr Ala		335
	340	345
Leu Gln Glu Ala Leu Lys Glu Lys Gln Gln His Ile Glu Gln Leu Leu		350
	355	360
Ala Glu Arg Asp Leu Glu Arg Ala Glu Val Ala Lys Ala Thr Ser His		365
	370	375
Val Gly Glu Ile Glu Gln Glu Leu Ala Leu Ala Arg Asp Gly His Asp		380
385	390	395
Gln His Val Leu Glu Leu Glu Ala Lys Met Asp Gln Leu Arg Thr Met		400
	405	410
Val Glu Ala Ala Asp Arg Glu Lys Val Glu Leu Leu Asn Gln Leu Glu		415
	420	425
Glu Glu Lys Arg Lys Val Glu Asp Leu Gln Phe Arg Val Glu Glu Glu		430
	435	440
Ser Ile Thr Lys Gly Asp Leu Glu Val Ala Thr Val Ser Glu Lys Ser		445
	450	455
Arg Ile Met Glu Leu Glu Lys Asp Leu Ala Leu Arg Val Gln Glu Val		460
465	470	475
Ala Glu Leu Arg Arg Arg Leu Glu Ser Asn Lys Pro Ala Gly Asp Val		480
	485	490
Asp Met Ser Leu Ser Leu Leu Gln Glu Ile Ser Ser Leu Gln Glu Lys		495
	500	505
Leu Glu Val Thr Arg Thr Asp His Gln Arg Glu Ile Thr Ser Leu Lys		510
	515	520
Glu His Phe Gly Ala Arg Glu Glu Thr His Gln Lys Glu Ile Lys Ala		525
	530	535
Leu Tyr Thr Ala Thr Glu Lys Leu Ser Lys Glu Asn Glu Ser Leu Lys		540
545	550	555
Ser Lys Leu Glu His Ala Asn Lys Glu Asn Ser Asp Val Ile Ala Leu		560
	565	570
Trp Lys Ser Lys Leu Glu Thr Ala Ile Ala Ser His Gln Gln Ala Met		575
	580	585
Glu Glu Leu Lys Val Ser Phe Ser Lys Gly Leu Gly Thr Glu Thr Ala		590
	595	600
Glu Phe Ala Glu Leu Lys Thr Gln Ile Glu Lys Met Arg Leu Asp Tyr		605
	610	615
Gln His Glu Ile Glu Asn Leu Gln Asn Gln Gln Asp Ser Glu Arg Ala		620
625	630	635
Ala His Ala Lys Glu Met Glu Ala Leu Arg Ala Lys Leu Met Lys Val		640
	645	650
		655



Ile Lys Glu Lys Glu Asn Ser Leu Glu Ala Ile Arg Ser Lys Leu Asp  
 660 665 670  
 Lys Ala Glu Asp Gln His Leu Val Glu Met Glu Asp Thr Leu Asn Lys  
 675 680 685  
 Leu Gln Glu Ala Glu Ile Lys Val Lys Glu Leu Glu Val Leu Gln Ala  
 690 695 700  
 Lys Cys Asn Glu Gln Thr Lys Val Ile Asp Asn Phe Thr Ser Gln Leu  
 705 710 715 720  
 Lys Ala Thr Glu Glu Lys Leu Leu Asp Leu Asp Ala Leu Arg Lys Ala  
 725 730 735  
 Ser Ser Glu Gly Lys Ser Glu Met Lys Lys Leu Arg Gln Gln Leu Glu  
 740 745 750  
 Ala Ala Glu Lys Gln Ile Lys His Leu Glu Ile Glu Lys Asn Ala Glu  
 755 760 765  
 Ser Ser Lys Ala Ser Ser Ile Thr Arg Glu Leu Gln Gly Arg Glu Leu  
 770 775 780  
 Lys Leu Thr Asn Leu Gln Glu Asn Leu Ser Glu Val Ser Gln Val Lys  
 785 790 795 800  
 Glu Thr Leu Glu Lys Glu Leu Gln Ile Leu Lys Glu Lys Phe Ala Glu  
 805 810 815  
 Ala Ser Glu Glu Ala Val Ser Val Gln Arg Ser Met Gln Glu Thr Val  
 820 825 830  
 Asn Lys Leu His Gln Lys Glu Glu Gln Phe Asn Met Leu Ser Ser Asp  
 835 840 845  
 Leu Glu Lys Leu Arg Glu Asn Leu Ala Asp Met Glu Ala Lys Phe Arg  
 850 855 860  
 Glu Lys Asp Glu Arg Glu Glu Gln Leu Ile Lys Ala Lys Glu Lys Leu  
 865 870 875 880  
 Glu Asn Asp Ile Ala Glu Ile Met Lys Met Ser Gly Asp Asn Ser Ser  
 885 890 895  
 Gln Leu Thr Lys Met Asn Asp Glu Leu Arg Leu Lys Glu Arg Asp Val  
 900 905 910  
 Glu Glu Leu Gln Leu Lys Leu Thr Lys Ala Asn Glu Asn Ala Ser Phe  
 915 920 925  
 Leu Gln Lys Ser Ile Glu Asp Met Thr Val Lys Ala Glu Gln Ser Gln  
 930 935 940  
 Gln Glu Ala Ala Lys Lys His Glu Glu Glu Lys Lys Glu Leu Glu Arg  
 945 950 955 960  
 Lys Leu Ser Asp Leu Glu Lys Lys Met Glu Thr Ser His Asn Gln Cys  
 965 970 975  
 Gln Glu Leu Lys Ala Arg Tyr Glu Arg Ala Thr Ser Glu Thr Lys Thr  
 980 985 990  
 Lys His Glu Glu Ile Leu Gln Asn Leu Gln Lys Thr Leu Leu Asp Thr  
 995 1000 1005  
 Glu Asp Lys Leu Lys Gly Ala Arg Glu Glu Asn Ser Gly Leu Leu Gln  
 1010 1015 1020  
 Glu Leu Glu Glu Leu Arg Lys Gln Ala Glu Lys Ala Lys Ala Ala Gln  
 1025 1030 1035 104  
 Thr Ala Glu Asp Ala Met Gln Ile Met Glu Gln Met Thr Lys Glu Lys  
 1045 1050 1055  
 Thr Glu Thr Leu Ala Ser Leu Glu Asp Thr Lys Gln Thr Asn Ala Lys  
 1060 1065 1070  
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 1075 1080 1085  
 Glu Glu Leu Asn Lys Ser Lys Glu Leu Leu Thr Val Glu Asn Gln Lys

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Met Glu Glu Phe Arg Lys Glu Ile Glu Thr Leu Lys Gln Ala Ala Ala		
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Gln Lys Ser Gln Gln Leu Ser Ala Leu Gln Glu Glu Asn Val Lys Leu		
1125	1130	1135
Ala Glu Glu Leu Gly Arg Ser Arg Asp Glu Val Thr Ser His Gln Lys		
1140	1145	1150
Leu Glu Glu Glu Arg Ser Val Leu Asn Asn Gln Leu Leu Glu Met Lys		
1155	1160	1165
Lys Arg Glu Ser Lys Phe Ile Lys Asp Ala Asp Glu Glu Lys Ala Ser		
1170	1175	1180
Leu Gln Lys Ser Ile Ser Ile Thr Ser Ala Leu Leu Thr Glu Lys Asp		
1185	1190	1195
Ala Glu Leu Glu Lys Leu Arg Asn Glu Val Thr Val Leu Arg Gly Glu		
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Asn Ala Ser Ala Lys Ser Leu His Ser Val Val Gln Thr Leu Glu Ser		
1220	1225	1230
Asp Lys Val Lys Leu Glu Leu Lys Val Lys Asn Leu Glu Leu Gln Leu		
1235	1240	1245
Lys Glu Asn Lys Arg Gln Leu Ser Ser Ser Ser Gly Asn Thr Asp Thr		
1250	1255	1260
Gln Ala Asp Glu Asp Glu Arg Ala Gln Glu Ser Gln Ile Asp Phe Leu		
1265	1270	1275
Asn Ser Val Ile Val Asp Leu Gln Arg Lys Asn Gln Asp Leu Lys Met		
1285	1290	1295
Lys Val Glu Met Met Ser Glu Ala Ala Leu Asn Gly Asn Gly Asp Asp		
1300	1305	1310
Leu Asn Asn Tyr Asp Ser Asp Asp Gln Glu Lys Gln Ser Lys Lys Lys		
1315	1320	1325
Pro Arg Leu Phe Cys Asp Ile Cys Asp Cys Phe Asp Leu His Asp Thr		
1330	1335	1340
Glu Asp Cys Pro Thr Gln Ala Gln Met Ser Glu Asp Pro Pro His Ser		
1345	1350	1355
Thr His His Gly Ser Arg Gly Glu Glu Arg Pro Tyr Cys Glu Ile Cys		
1365	1370	1375
Glu Met Phe Gly His Trp Ala Thr Asn Cys Asn Asp Asp Glu Thr Phe		
1380	1385	1390

&lt;210&gt; 815

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 815

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catcaagcgc	ttcgagcaga	agggattccg	cctcgtggcc	atgaagttcc	tccgggcctc	180
tgaagaacac	ctgaagcagc	actacattga	cctgaaaagac	cgaccattct	tccctgggct	240
ggtgaagtac	atgaactcag	ggccggttgt	ggccatggtc	tgggaggggc	tgaacgtggt	300
gaagacaggc	cgagtgatgc	ttggggagac	caatccagca	gattcaaaagc	caggcaccat	360
tcgtggggac	ttctgcattc	aggttggcag	gaacatcatt	catggcagtg	attcagtaaa	420
aagtgcgtgaa	aaagaaatca	gcctatgggt	taagcctgaa	gaactgggtg	actacaagtc	480
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ggcgtggtgt	gtccctggac	acagctcttc	attccattga	cttagaggca	acaggattga	600
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 Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu  
 35 40 45  
 Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu  
 50 55 60  
 Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly  
 65 70 75 80  
 Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro  
 85 90 95  
 Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val  
 100 105 110  
 Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys  
 115 120 125  
 Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp Tyr Lys Ser  
 130 135 140  
 Cys Ala His Asp Trp Val Tyr Glu  
 145 150

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